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Dissemination models: applications in epidemiology, rumour spreading, wealth distribution, and opinion formation

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Chapter 4

Demography, contacts, and severity

Chapter overview

In many societies, populations are ageing. We ask how shifts in demography modify contact patterns and, as a consequence, the potential for severe outbreaks, measured by the basic reproduction number R_0 and the final size. We study a deterministic multi-type SIR model and examine representative ways in which contacts can depend on population size and composition, subject to reciprocity (contacts are mutual). Although we motivate the analysis using age groups, ‘group’ is generic and may represent any partition of the population (e.g., by occupation, behaviour or geography). For the considered demography-dependent contact patterns we provide theoretical results describing how R_0 and the final size vary with demography. In the age-structured interpretation, for a contact pattern in which the group of young agents—who maintain a fixed contact rate—shrinks (an ageing shift), we show that R_0 decreases and the fraction of susceptibles remaining after the outbreak increases.

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4.1 Introduction

Across many countries, national statistical offices project continued population ageing over the coming decades — for example, Japan, the UK, and the Netherlands each anticipate higher proportions of older adults [121, 150, 158]. Such ageing can cause challenges ranging from increased public-health burden to a lack of workforce. Yet, despite its relevance for designing intervention strategies, the impact of ageing on the severity of epidemic outbreaks (of *short duration*, relative to demographic change) has received relatively little attention in the literature [113, 114]. In this chapter we will theoretically examine how demographic change alters contact patterns and, in turn, how these changes affect epidemic severity measures.

Separation of timescales

As noted above, we will consider outbreaks that unfold on timescales much shorter than those of demographic change. Seasonal influenza is a typical example: an outbreak usually lasts only a few months, whereas ageing operates on the scale of decades [169]. For this reason, we will assume that population size and composition are constant during an outbreak.

Under this assumption, we study a deterministic multi-type SIR framework. Having multiple types allows us to represent a partition of the population into groups, such as age groups. However, although age is the key use case of our framework, throughout this chapter the term ‘group’ is generic and may represent any partition of the population. For example, groups may be defined by occupation (e.g., high-contact versus low-contact jobs), behaviour (e.g., hygiene practices or attitudes towards vaccination), or geography (e.g., living near or far from the initial outbreak). We examine how severity measures, such as the final size and the basic reproduction number, change in response to shifts in population size and composition. Formal definitions of these measures are provided in Section 4.2.4; informally, the final size is the number of individuals who become infected over the course of the outbreak, and the basic reproduction number is the average number of new infections caused by a single infectious individual during the earliest phase of an outbreak.

Demography-dependent contact patterns

A key ingredient in our analysis is how shifts in demography alter contact patterns. We consider a range of demography-dependent contact patterns that typically satisfy the reciprocity condition (contacts are mutual). We distinguish two main classes: *frequency dependence*, in which contact patterns depend only on population composition and not on population size; and *density dependence*, in which contact patterns depend on both size and composition. In single-type models these distinctions have been extensively discussed (e.g., [18, 112]). Nonetheless, in multi-type models there is no consensus on which contact patterns should be termed ‘frequency’ or ‘density’ dependent. In general, the most appropriate description of a contact pattern depends on the population and pathogen under study [89, 144].

Contributions

Our contribution is threefold. First, while deterministic multi-type SIR models are classical (see, e.g., [52, 53, 79]), we set up a framework in which the contact matrix is an explicit function of demography. This provides an analytically tractable mapping from population structure to contact structure and, in turn, to epidemic severity measures. Second, we introduce and organise several families of demography-dependent contact patterns, capturing multiple mechanisms by which contact rates may adjust when population size or composition changes. Third, building on this framework and catalogue, we derive qualitative sensitivity results describing how demographic perturbations affect the basic reproduction number R_0 and the final size.

More broadly, our study provides an analytical approach to assess when homogeneous (single-type) approximations can misrepresent epidemic severity under demographic change.

Organisation of chapter

The chapter is organised as follows. Section 4.2 introduces the model and discusses key ingredients, and model properties. Section 4.3 discusses ways in which contact patterns can depend on demography. Section 4.4 presents the main theoretical results, with proofs collected in Section 4.5. We end with a discussion in Section 4.6.

4.2 Model and properties

4.2.1 Demography

As mentioned in the introduction, our aim in this chapter is to develop a theoretical understanding of how the severity of an epidemic outbreak depends on demographic change — such as population ageing — through its effect on contact structures. Specifically, we study outbreaks on relatively short timescales (typically less than two years) and ask how their severity varies with demographic changes, occurring over much longer timescales. This difference in timescales motivates a key simplification: we treat demography (and the contact structure it induces) as constant over the course of a single outbreak. To make this precise, we first clarify what we mean by *demography*. Throughout, we use the following definitions.

Definition 4.2.1 (Demography). *Let $N > 0$ denote the total number of individuals; we refer to N as the **population size**. We assume that the population is partitioned into $m \geq 1$ groups (e.g., age, occupation, behaviour, or geography). For each type i , let $N_i \geq 0$ be its number of individuals, so that $\sum_{i=1}^m N_i = N$; we call N_i the **population size of type i** . From these group sizes we define the **population fractions** $n_i := N_i/N \in [0, 1]$, which satisfy $\sum_{i=1}^m n_i = 1$. These fractions form the **population composition** vector $\mathbf{n} := (n_1, \dots, n_m)^\top$. Combining the population size and the composition yields the vector $\mathbf{N} := N\mathbf{n} = (N_1, \dots, N_m)^\top$, which we call the **demography** of the population.*

To study how the severity of an epidemic outbreak depends on changes in the demographic vector $\mathbf{N}$, we require an epidemic model that partitions the population into m types. To

examine this dependence while preserving only the essential mechanisms, and to keep the mathematics tractable, we work in a fluid-limit (deterministic mean-field) framework and describe the classical multi-type SIR formulation.

4.2.2 Model

As announced in Section 4.2.1, we use a classical multi-type SIR model [52, 53, 79] as a baseline framework for structured-population dynamics. We consider a population partitioned into m types with demography $\mathbf{N} = (N_1, N_2, \dots, N_m)^\top$. From an epidemiological perspective, each type is divided into three epidemic states: *Susceptible* (individuals who can become infectious after effective contact with an infectious individual), *Infectious* (individuals who can transmit infection to susceptibles), and *Recovered* (individuals who were infectious and cannot become infectious again). For each type i , we denote the numbers in these states by S_i , I_i , and R_i , respectively, with the conservation law $S_i + I_i + R_i = N_i$.

The partitioning of the population into m types allows transition rates to be type-specific. We will let these transition rates depend on the demography $\mathbf{N}$ via the contact-rate parameter, defined as follows.

Definition 4.2.2 (Model parameters). *We denote by $k_{ij}(\mathbf{N})$ the average number of contacts per unit of time that a type- j individual has with type- i individuals; this number may depend on the demography $\mathbf{N}$. We denote the matrix with contact rates as a **contact pattern**:*

$$\mathbf{K}(\mathbf{N}) = (k_{ij}(\mathbf{N}))_{1 \leq i, j \leq m}.$$

Given a contact between an infectious type- j individual and a susceptible type- i individual, let $p_{ij} \in [0, 1]$ be the probability that the susceptible becomes infectious. Combining these, define

$$\beta_{ij}(\mathbf{N}) := p_{ij} k_{ij}(\mathbf{N}),$$

interpreted as the average number of new infections per unit time in group i caused by a single infectious individual in group j , given that all individuals of type- i are susceptible¹. The matrix of these β -rates is denoted by

$$\mathbf{B} =: (\beta_{ij}(\mathbf{N}))_{1 \leq i, j \leq m},$$

and the matrix of p_{ij} is denoted by $\mathbf{P} := (p_{ij})_{1 \leq i, j \leq m}$. Finally, let $\alpha_i > 0$ denote the recovery rate of type- i infectious individuals and $\boldsymbol{\alpha} := (\alpha_1, \dots, \alpha_m)^\top$.

Remark 4.2.3. *In this chapter, the contact rates $k_{ij}(\mathbf{N})$ are treated as given nonnegative functions of the demography $\mathbf{N}$. Specific demography-dependent families of contact patterns used in this chapter are introduced in Section 4.3.*

As illustrated in Figure 4.1, we aim to model how individuals of type i progress through the epidemic states susceptible, infectious, and recovered.

¹Here we take p_{ij} to be independent $\mathbf{N}$ and focus solely on the impact of demography through the contact-rate parameter

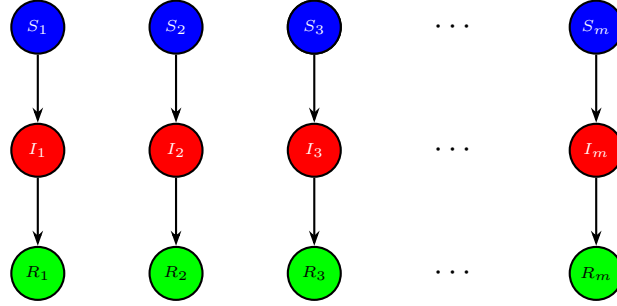


Figure 4.1: Scheme of the possible transitions in a multi-type SIR model with m -types

The additional ingredient in the multi-type SIR model relative to the standard SIR model is that infectiousness — captured by the coefficients β_{ij} — depends on the types of both the infective j and the susceptible i .

We now derive the coupled system of ODEs corresponding to the fluid-limit multi-type SIR model, by combining the components introduced above in an interpretative manner. Recall that $\beta_{ij} \geq 0$ denotes the average number of new infections per unit time in group i caused by a single infectious individual from group j , when all type- i individuals are susceptible. During an outbreak, however, there are $I_j(t)$ infectious individuals and only a fraction S_i/N_i of group i remains susceptible. Thus, the rate at which susceptibles of type i are infected by type- j infectious individuals is $\frac{S_i(t)}{N_i} \beta_{ij}(\mathbf{N}) I_j(t)$. Summing over all types $j \in \{1, 2, \dots, m\}$ and recalling that the recovery rate of a type- i infectious individual is $\alpha_i > 0$ we arrive at the following description for the multi-type SIR model

$$\begin{aligned} \frac{dS_i}{dt} &= -\frac{S_i}{N_i} \sum_{j=1}^m \beta_{ij}(\mathbf{N}) I_j \\ \frac{dI_i}{dt} &= \frac{S_i}{N_i} \sum_{j=1}^m \beta_{ij}(\mathbf{N}) I_j - \alpha_i I_i, \\ \frac{dR_i}{dt} &= \alpha_i I_i, \end{aligned} \tag{4.1}$$

with $S_i(t) + I_i(t) + R_i(t) = N_i$ for $t \in \mathbb{R}$ and $i \in \{1, 2, \dots, m\}$. Regarding the initial condition, we leave the introduction time of the pathogen implicit, requiring only that in the distant past the population is fully susceptible: $(S_i(-\infty), I_i(-\infty), R_i(\infty)) := \lim_{t \downarrow -\infty} (S_i(t), I_i(t), R_i(t)) = (N_i, 0, 0)$.

4.2.3 Demography-dependent contact pattern $\mathbf{K}(\mathbf{N})$

In this subsection we take a closer look at the contact pattern $\mathbf{K}$, which depends on the demography $\mathbf{N}$. To illustrate the pattern itself, Figure 4.2 shows how the contact rates k_{ij} encode interactions between types, including within-type contacts in a 3-type model.

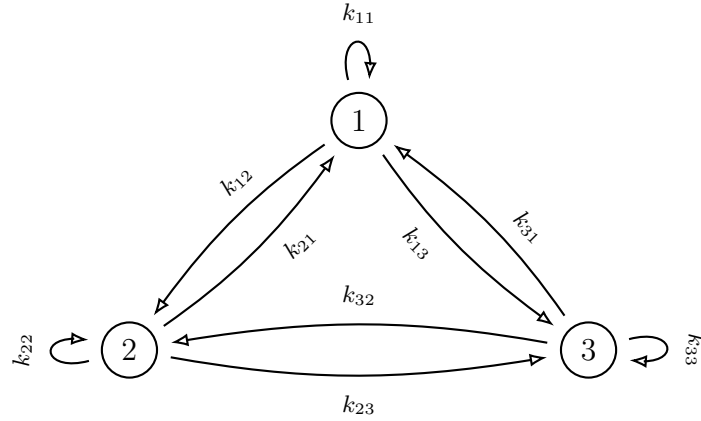


Figure 4.2: Scheme of the contact rates k_{ij} in a 3-type system. The number in each node denotes its type. The contact rate next to an arrow shows the relevant k_{ij} .

In what follows, we exclude degenerate cases in which the population separates, from a contact perspective, into disjoint components. In particular, any two individuals can be linked by a finite chain of contacts. Formally, we assume the following.

Assumption 4.2.4 (Irreducibility of $\mathbf{K}$). *The contact pattern $\mathbf{K}$ is irreducible, i.e., for every pair $i, j \in \{1, 2, \dots, m\}$ there exists an integer l_{ij} such that $(\mathbf{K}^{l_{ij}})_{ij} > 0$.*

With Assumption 4.2.4 in place, we examine scenarios of how demographic change — such as population ageing — alters the contact pattern $\mathbf{K}$ and, through it, the severity of an outbreak as measured by R_0 and the final size $1 - \sigma$. (both defined in Section 4.2.4). This chain of dependence can be summarised as

$$\mathbf{N} \mapsto \mathbf{K}(\mathbf{N}) \mapsto (1 - \sigma(\mathbf{K}(\mathbf{N})), R_0(\mathbf{K}(\mathbf{N}))),$$

where each arrow indicates functional dependence on the preceding quantity.

To make the $\mathbf{N} \mapsto \mathbf{K}$ mapping explicit, Section 4.3 provides a list of classes of demography-dependent contact patterns. Our main results then examine how perturbations in $\mathbf{N}$ propagate to σ and R_0 , with particular attention to implications for ageing. The next subsection formally introduces the notions of final size and the basic reproduction number R_0 .

4.2.4 Epidemic severity: final size and R_0

In this subsection we introduce the notions of final size and the basic reproduction number, R_0 , as measures of the severity of an epidemic outbreak. Note that the convergence of $S_i(t)$ as $t \rightarrow \infty$ follows from monotonicity and boundedness. Informally, by final size we mean ‘how many individuals’ are infected over the course of the outbreak. We formalise this in the following definition.

Definition 4.2.5 (Final size). *Let $S_i(\infty) := \lim_{t \rightarrow \infty} S_i(t)$ for $i \in \{1, \dots, m\}$, and write $\mathbf{S}(\infty) := (S_1(\infty), \dots, S_m(\infty))^\top$. Define for group i*

$$R_i(\infty) := N_i - S_i(\infty),$$

we write $\mathbf{R} := (R_1(\infty), \dots, R_m(\infty))^\top$. Next, define the fraction of susceptibles remaining in group i at the end of the outbreak by

$$\sigma_i := \frac{S_i(\infty)}{N_i},$$

and call $1 - \sigma$ the **fractional final size**, with $\sigma := (\sigma_1, \dots, \sigma_m)^\top$. Finally, we denote by $\mathbf{R}/N$ the **normalised total final size**.

Final size equations and probabilistic interpretation

The term σ in the fractional final size admits an explicit relation with the transmission rates $\mathbf{B}$, the demography $\mathbf{N}$, and the recovery rates α (see Definitions 4.2.1 and 4.2.2). Starting from (4.1) and using the conditions $S_i(-\infty) = N_i$, $I_i(\infty) = I_i(-\infty) = 0$, we obtain

$$\log(S_i(\infty)) - \log(N_i) = \int_{-\infty}^{\infty} \frac{dS_i(t)}{dt} \frac{1}{S_i(t)} dt = -\frac{1}{N_i} \sum_{j=1}^m \beta_{ij} \int_{-\infty}^{\infty} I_j(t) dt, \quad (4.2)$$

and

$$-\alpha_i \int_{-\infty}^{\infty} I_i(t) dt = \int_{-\infty}^{\infty} \frac{dS_i(t)}{dt} + \frac{dI_i(t)}{dt} dt = S_i(\infty) - N_i, \quad (4.3)$$

for all $i \in \{1, \dots, m\}$. Combining these identities yields the so-called final size equations,

$$\sigma_i = \exp \left[\sum_{j=1}^m \frac{\beta_{ij}}{\alpha_j} \frac{N_j}{N_i} (\sigma_j - 1) \right], \quad i = 1, \dots, m. \quad (4.4)$$

The final size equations (4.4) admit a natural *probabilistic interpretation*. The probability that a given type- i susceptible escapes infection over the whole outbreak is σ_i (so $1 - \sigma_i$ is the infection probability). For a single individual exposed to a time-varying *force of infection* $\lambda_i(t)$ per unit of time — that is integrable over the outbreak period — the escape probability is

$$\sigma_i = \exp \left(- \int_{-\infty}^{\infty} \lambda_i(t) dt \right).$$

It is thus convenient to write $\sigma_i = \exp(-C_i)$ with $C_i := \int_{-\infty}^{\infty} \lambda_i(t) dt$ the *cumulative force of infection* on a type- i individual. In our multi-type SIR model we have from (4.1),

$$\lambda_i(t) = \frac{1}{N_i} \sum_{j=1}^m \beta_{ij} I_j(t),$$

so C_i is the cumulative force of infection accumulated over the course of the outbreak on a single individual. To express C_i in terms of model parameters *only*, we analyse the force of infection that a single infectious type- j individual generates during its infectious period. For this, note that a single infectious type- j individual generates β_{ij} new infections per unit of time in group i when all type- i individuals are susceptible. Therefore, it contributes a force of infection β_{ij}/N_i per unit of time to any type- i individual. Over its infectious lifetime with expected duration $1/\alpha_j$, the total force of infection contributed by that one

type- j infectious individual is therefore $\beta_{ij}/(N_i\alpha_j)$. Over the entire outbreak, the number of type- j individuals who ever become infectious is $(1 - \sigma_j)N_j$. Summing the contributions of all such individuals gives

$$C_i = \sum_{j=1}^m \frac{\beta_{ij}}{N_i\alpha_j} (1 - \sigma_j) N_j = \sum_{j=1}^m \frac{\beta_{ij}}{\alpha_j} \frac{N_j}{N_i} (1 - \sigma_j).$$

Combining this with $\sigma_i = \exp(-C_i)$ yields the final-size equations (4.4).

The basic reproduction number (R_0)

Another measure of outbreak severity used in this chapter is the basic reproduction number, R_0 , informally interpreted as the average number of new infections due to a single infectious individual at the earliest phase of the epidemic.

In the multi-type SIR model considered here, we define R_0 as the dominant eigenvalue of the next generation matrix (NGM) [52]. The (i, j) entry of the NGM is the average number of new infections in group i due to a single infectious individual from group j when all type- i individuals are susceptible (as at the earliest phase of the epidemic). To connect this definition to model parameters, observe that a type- j infectious individual has k_{ij} contacts per unit of time with type- i individuals, each contact resulting in infection with probability p_{ij} . Consequently, when all type- i individuals are susceptible, the average infections per unit of time in group i caused by one type- j infectious individual is $\beta_{ij} = p_{ij}k_{ij}$. With mean infectious duration $1/\alpha_j$ for type- j infectious individuals we arrive at the following definition.

Definition 4.2.6 (Next generation matrix (NGM) and basic reproduction number (R_0)).
The *next generation matrix* M is

$$\mathbf{M}(\mathbf{N}) = \begin{pmatrix} \frac{p_{11}k_{11}(\mathbf{N})}{\alpha_1} & \dots & \frac{p_{1m}k_{1m}(\mathbf{N})}{\alpha_m} \\ \vdots & \ddots & \vdots \\ \frac{p_{m1}k_{m1}(\mathbf{N})}{\alpha_1} & \dots & \frac{p_{mm}k_{mm}(\mathbf{N})}{\alpha_m} \end{pmatrix}, \quad (4.5)$$

where the elements of $\mathbf{M}(\mathbf{N})$ are $m_{ij} \geq 0$. The **basic reproduction number** is the dominant eigenvalue of M

$$R_0(\mathbf{N}) := \rho(\mathbf{M}(\mathbf{N})), \quad (4.6)$$

where $\rho(\cdot)$ denotes the dominant eigenvalue of a square matrix.

For $m = 1$, the NGM has the single entry $\beta_{11}(\mathbf{N})/\alpha_1$, and hence $R_0 = \beta_{11}(\mathbf{N})/\alpha_1$, as expected for the homogeneous SIR model. Note that under Assumption 4.2.4, and provided that $p_{ij} > 0$ whenever $k_{ij}(\mathbf{N}) > 0$, the matrix $\mathbf{M}(\mathbf{N})$ is irreducible as well. We emphasise the dependence on the demography $\mathbf{N}$ through the notation $\mathbf{M}(\mathbf{N})$ and $R_0(\mathbf{N})$.

As expected from interpretation, an outbreak occurs only if a single infectious individual in the earliest phase causes, on average, strictly more than one new infection. This is formalised in Theorem 4.4.1. Conversely, in the late phase of the epidemic the average number of new infections caused by a single individual is strictly less than one, marking

that the epidemic is ending (this is made precise in Lemma 4.4.2). With the model and necessary ingredients in place, we now examine demography-dependent contact patterns before we analyse how the final size and the basic reproduction number depend on changes in the demography $\mathbf{N}$.

Remark 4.2.7. *Note that the measures used here — final size and R_0 — do not account for hospitalisation or mortality. They are therefore insufficient, on their own, to support conclusions about public-health burden.*

4.3 Catalogue of demography-dependent contact patterns

In this section we discuss — and offer an initial catalogue of — demography-dependent contact patterns, without claiming completeness. We distinguish two broad classes. The first comprises *frequency dependent* contact patterns, which depend only on the population composition $\mathbf{n}$ and not on the total size N . The second comprises *density dependent* contact patterns, which are those that are not frequency dependent and therefore do depend on N . We note that in the literature there is no general consensus on which contact patterns fall under ‘frequency’ or ‘density’ dependence in a multi-type model.

Before turning to these classes, we introduce the *reciprocity condition*. In human interaction, contacts are typically reciprocal: if person A has contact with person B , then person B has contact with person A as well. Mathematically, reciprocity is expressed as

$$k_{ij} N_j = k_{ji} N_i, \quad (4.7)$$

meaning that the total number of contacts per unit of time from type j to type i equals the total from type i to type j . Since we are primarily interested in human (physical) interactions, we assume throughout — unless stated otherwise — that a contact pattern satisfies the reciprocity condition (4.7).

For clarity, we first provide a summary of the contact patterns treated in this chapter. In the frequency dependent class we consider *proportionate mixing*, *bilateral contact patterns*, *(bilateral) domination contact patterns*, and *power contact patterns*. To distinguish them notationally we use superscripts on $\mathbf{K}$ and k_{ij} : prop, b, bd, and p, respectively. In the density dependent class we discuss the linear density dependent pattern, denoted by the superscript d. Table 4.1 summarises these demography-dependent contact patterns and indicates whether the reciprocity condition (4.7) holds.

Table 4.1: List of demography-dependent contact patterns treated in this chapter.

Contact pattern	Notation	Reciprocity (4.7)	Remarks
Frequency dependence			
Proportionate mixing	k_{ij}^{prop}	Yes	
Bilateral contact patterns	k_{ij}^{b}	Yes	
Domination (bilateral) contact patterns	k_{ij}^{bd}	Yes	subclass of bilateral
Power contact patterns	k_{ij}^{p}	for $d = 1/2$	
Density dependence			
Linear density dependent contact patterns	k_{ij}^{d}	Yes	

4.3.1 Frequency dependence

We start with a typical example to provide intuition for what frequency dependence means in practice. Seals resting on a sandbank tend to lie at a roughly fixed distance from each other. Thus, when a new seal joins the sandbank population (in our model terms, N increases to $N + 1$), the distance between neighbouring seals does not change. Interpreting this distance as a proxy for the contact rate, we conclude that the contact pattern is independent of population size. This classic example of a frequency dependent contact pattern was studied in [45, 49]. In this chapter we define a demography-dependent contact pattern *frequency dependent* as follows.

Definition 4.3.1 (frequency dependence). *If $\mathbf{K}$ is independent of the population size N , that is, $\mathbf{K}(N) = \mathbf{K}(\alpha N)$ for any $\alpha > 0$, then we call $\mathbf{K}$ a **frequency dependent** contact pattern.*

We now introduce several frequency dependent contact patterns, without claiming completeness (see Table 4.1 for an overview).

Proportionate mixing

In everyday life, contacts often arise as opportunistic encounters in shared settings (e.g., classrooms, workplaces and public transport)—so the chance of meeting someone from a given group depends on how much that group is ‘present’ in such settings. To capture this in mathematical notation, suppose that a type- i individual contributes $c_i > 0$ units of contact availability (or social activity) per unit time. Then the total contact availability of group i is proportional to $c_i N_i$, and a randomly encountered contact partner is of type i with probability $c_i N_i / \sum_{s=1}^m c_s N_s$ under the assumption of uniform mixing.

Assume, moreover, that a type- j individual has a fixed number of contacts per unit of time, $c_j > 0$. We call a demography-dependent contact pattern *proportionate mixing* when the fraction of a type- j individual’s contacts made with group i is *proportional* to that group’s total contact per unit time: $c_i N_i$ [16]. For proportionate mixing the elements of $\mathbf{K}$ are

$$k_{ij}^{\text{prop}} = \frac{c_i N_i}{\sum_{s=1}^m c_s N_s} c_j, \quad i, j \in \{1, \dots, m\}, \quad (4.8)$$

By construction, we have $\sum_{i=1}^m k_{ij}^{\text{prop}} = c_j$ for each j . Clearly, k_{ij}^{prop} does not depend on the total population size N and it satisfies the reciprocity condition (4.7). An important characteristic of proportionate mixing is that changing N_z for any z affects all k_{ij}^{prop} , including those that do not involve group z ; this contrasts with bilateral patterns as discussed in the next subsection. An advantage of proportionate mixing is that it allows us to think intuitively about the demography-dependent contact pattern. However, an important disadvantage is that it does not allow specific pairs of groups to have a specific number of contacts per unit time — required, for example, when modelling differences in contacts between children and parents, or between grandchildren and grandparents.

Bilateral contact patterns

Many interactions in human populations are shaped by obligations that connect two groups. An illustrative example is caregiving. Children require regular contact with caregivers (parents, teachers, childcare staff), while older adults may require contacts with carers, family members, or health professionals. When the size of one such group changes, the other group typically adapts its time towards that group: if there are more children, caregivers divide their attention more; if there are fewer children, the same caregivers may spend more time per child or redirect effort elsewhere. Importantly, these adjustments are driven *only* by the sizes of the two groups involved. This motivates the following contact pattern.

We speak of a *bilateral* contact pattern if the contact rate k_{ij} of a type- j individual with type- i individuals depends *only* on N_i and N_j , but not on N_k for $k \notin \{i, j\}$. This is somewhat related to pair-formation models; see [75].

Linear bilateral contact patterns

In this chapter we only consider the class of *linear* bilateral contact patterns. We fix a pair of groups (i, j) and assume that the contact rates belong to a special class of frequency dependent patterns² of the form (with $A, B, C, D \geq 0$)

$$k_{ij}(N_i, N_j) = \frac{AN_i + BN_j}{CN_i + DN_j} = q \frac{aN_i + (1-a)N_j}{cN_i + (1-c)N_j}, \quad (4.9)$$

where $q = \frac{A+B}{C+D}$, $a = \frac{A}{A+B}$, and $c = \frac{C}{C+D}$. The parameters q, a, c may (and typically will) depend on the ordered pair (i, j) ; later we write q_{ij} and c_{ij} to reflect this. Similarly, for k_{ji} , with $\tilde{A}, \tilde{B}, \tilde{C}, \tilde{D} \geq 0$,

$$k_{ji}(N_i, N_j) = \frac{\tilde{A}N_j + \tilde{B}N_i}{\tilde{C}N_j + \tilde{D}N_i} = \tilde{q} \frac{\tilde{a}N_j + (1-\tilde{a})N_i}{\tilde{c}N_j + (1-\tilde{c})N_i}, \quad (4.10)$$

where $\tilde{q} = \frac{\tilde{A}+\tilde{B}}{\tilde{C}+\tilde{D}}$, $\tilde{a} = \frac{\tilde{A}}{\tilde{A}+\tilde{B}}$, and $\tilde{c} = \frac{\tilde{C}}{\tilde{C}+\tilde{D}}$. The reciprocity condition (4.7) becomes

$$q \frac{aN_i + (1-a)N_j}{cN_i + (1-c)N_j} N_j = \tilde{q} \frac{\tilde{a}N_j + (1-\tilde{a})N_i}{\tilde{c}N_j + (1-\tilde{c})N_i} N_i. \quad (4.11)$$

²There are also bilateral patterns that are not linear. For instance, $k_{ij} = N_i \frac{aN_i + bN_j}{AN_i^2 + 2BN_iN_j + CN_j^2}$ and $k_{ji} = N_j \frac{aN_i + bN_j}{AN_i^2 + 2BN_iN_j + CN_j^2}$ satisfy reciprocity (4.7), are frequency dependent, and depend only on N_i, N_j .

Since (4.11) must hold for all $N_i, N_j \geq 0$, setting $N_i = N_j > 0$ yields $q = \tilde{q}$.

Four cases of linear bilateral contact patterns

In what follows we analyse (4.11) (under $q = \tilde{q}$) by separating cases according to whether c and $\tilde{c}$ are zero or nonzero.

Case 1: $c \neq 0$ and $\tilde{c} \neq 0$. Setting $N_j = 0$ in (4.11) forces $\tilde{a} = 1$; similarly, setting $N_i = 0$ we find that necessarily $a = 1$. With these, the numerators are equal, and equality of denominators then requires $\tilde{c} = 1 - c$. Hence

$$k_{ij} = q \frac{N_i}{cN_i + (1-c)N_j}, \quad k_{ji} = q \frac{N_j}{cN_i + (1-c)N_j}. \quad (4.12)$$

Case 2: $c = 0$ and $\tilde{c} = 0$. Substituting into (4.11) gives $\tilde{a} = 1 - a$, so

$$k_{ij} = q \frac{aN_i + (1-a)N_j}{N_j}, \quad k_{ji} = q \frac{aN_i + (1-a)N_j}{N_i}. \quad (4.13)$$

Case 3: $c = 0$ and $\tilde{c} \neq 0$. As above, one finds $a = 1$ and $\tilde{a} = \tilde{c}$, yielding

$$k_{ij} = q \frac{N_i}{N_j}, \quad k_{ji} = q. \quad (4.14)$$

Case 4: $c \neq 0$ and $\tilde{c} = 0$. By symmetry,

$$k_{ij} = q, \quad k_{ji} = q \frac{N_j}{N_i}. \quad (4.15)$$

Note that, apart from q , the families in Cases 1 and 2 each have one free parameter, and Cases 3 and 4 form the boundary between Cases 1 and 2 (indeed, in Case 1 letting $c \in \{0, 1\}$ yields Cases 3 and 4; similarly, in Case 2 take $a \in \{0, 1\}$). In Case 2 the contact rate can become arbitrarily large, in contrast to Case 1. We therefore define the bilateral contact pattern by Case 1, with Cases 3 and 4 as its boundary cases:

$$k_{ij}^b = q_{ij} \frac{N_i}{c_{ij}N_i + (1-c_{ij})N_j}. \quad (4.16)$$

In the following subsection, we discuss a special bilateral linear contact pattern, where we allow c_{ij} to only take the values 0 or 1 (hence arriving in Cases 3 or 4).

Domination (bilateral) contact patterns

We continue the ‘caregiving’ narrative used above, and now specify it to situations in which one side effectively fixes their contact rate while the other side adjusts. In childcare, especially for infants, interactions are often driven by non-negotiable needs (e.g., feeding, nappy changes or help with dressing) so it can be reasonable to model each child as requiring a roughly fixed amount of caregiver contact per unit time. When the number

of children changes, the adjustment is then primarily borne by caregivers. In this sense, children dominate their parents/caregivers.

By contrast, for care of older adults the direction of ‘who sets the terms’ can plausibly reverse. In many settings, healthcare staff have fixed capacities and protocols that determine how many visits they provide per unit time. If the number of older adults changes, each older adult may receive more or fewer contacts depending, but the per-carer contact rate can remain constant. In this sense, caregivers dominate the elderly.

This ‘one side fixes, the other adjusts’ mechanism corresponds precisely to the boundary cases of the linear bilateral family (Cases 3 and 4), where $c_{ij} \in \{0, 1\}$ (see (4.16)). Let us focus on Case 4: here the number of contacts that a type- j individual makes with type- i individuals is independent of the population composition. Thus, type- j individuals keep their contacts with group i fixed per unit time, while type- i individuals adjust their contacts with group j accordingly. In this situation we say that group j *dominates* group i .

Definition 4.3.2 (Domination). *We say that group j **dominates** group i if and only if $c_{ij} = 1$ (and therefore $c_{ji} = 0$, see (4.16)). A pair of groups (i, j) is a **domination pair** if either group i dominates group j or group j dominates group i . A bilateral contact pattern is a **domination contact pattern** if each pair of groups in the population is a domination pair.*

*A group i is **royal** if it dominates all other groups in the population. Similarly, a group i is **servant** if every other group dominates group i .*

Note that a domination contact pattern need not contain a royal or a servant group, and conversely, a bilateral contact pattern with a royal or a servant group need not be a domination contact pattern. In Section 4.4.2 we shall assume that the group of children dominates the middle-aged (parents) and the aged (grandparents) (a royal group), while the aged form a servant group.

Power contact patterns

A concrete example for the power family comes from organised sports. Consider a training programme in which group i consists of players and group j consists of coaches. Interpret a ‘contact’ as a brief close-range coaching interaction (instruction or feedback). Recall that k_{ij} denotes the average number of contacts per unit time that a type- j individual has with type- i individuals.

How should k_{ij} respond when the numbers of players or coaches change? There are at least two plausible regimes. If a coach tries to check in with many players each session, then increasing the number of players N_i while keeping the number of coaches N_j fixed can lead to each coach interacting with more players per unit time, so k_{ij} increases with N_i . In contrast, if coaches cannot increase their total number of interactions, then increasing N_i at fixed N_j forces prioritisation, so the number of player-interactions per coach may decrease. Similarly, increasing the number of coaches N_j at fixed N_i can either decrease each coach’s contact count (more coaches share the same players), or increase it if smaller group sizes allow more frequent check-ins per coach. The direction therefore depends on how the programme organises training.

The power family provides a compact way to represent such scaling behaviours. If we model the dependence on relative group size by a power law in the ratio N_i/N_j , then the sign of the exponent d captures the direction of the effect. The magnitude $|d|$ determines how strongly contacts respond to changes in relative group sizes, and the special case $d = 0$ corresponds to no demographic dependence (the power family is related to gravity models, e.g., [21, 173]).

Formalising this, we define the power contact pattern as

$$k_{ij}^p = q_{ij}^p \left(\frac{N_i}{N_j} \right)^d, \quad (4.17)$$

with $q_{ij}^p = q_{ji}^p > 0$ and $d \in \mathbb{R}$. Note that k_{ij}^p is independent of the total population size N (hence frequency-dependent), and it satisfies the reciprocity condition (4.7) only when $d = \frac{1}{2}$.

For $d = 1$, the number of contacts per unit time that a type- j individual makes with type- i individuals is inversely proportional to the size of group j ; hence the *total* number of contacts per unit time from group j to group i equals $k_{ij}^p N_j = q_{ij}^p N_i$, which is independent of N_j .

From a mathematical point of view, this family is convenient. We will show in Theorem 4.4.8 that, in a model with the demography-dependent power contact pattern, the basic reproduction number is independent of the composition $\mathbf{n}$ for all $d \in \mathbb{R}$. In addition, when $d = 1$, the fractional final size is also independent of the population composition.

4.3.2 Density dependence

As with frequency dependence, we first illustrate density dependence by an example. Imagine a swimming pool of fixed size with an increasing number of swimmers. We assume that the number of contacts per unit time increases as the distance between individuals decreases. As the number of swimmers grows, the area available per swimmer shrinks, reducing the distance between swimmers and thereby increasing the contact rate per unit time (this is essentially the law of mass action from chemical kinetics).

In general, we say that a contact pattern is *density dependent* if the number of contacts per unit time that a type- j individual makes with type- i individuals depends not only on the composition $\mathbf{n}$ but also on the total population size N (see, e.g., [79] and Section 12.2 of [50]).

Definition 4.3.3 (Density dependence). *If $\mathbf{K}$ depends on the population size N , that is, $\mathbf{K}(N) \neq \mathbf{K}(\alpha N)$ for some $\alpha > 0$, then we call $\mathbf{K}$ a **density dependent** contact pattern.*

Linear density dependent contact patterns

In this chapter we consider a narrower class of density dependent patterns. We assume that the number of contacts per unit of time that a type- j individual makes with type- i individuals is linear in the size of group i . Thus the entries of $\mathbf{K}$ are

$$k_{ij}^d = q_{ij}^d N_i, \quad (4.18)$$

with $q_{ij}^d = q_{ji}^d > 0$, in order to satisfy the reciprocity condition (4.7). The total number of contacts per unit time made by a type- j individual is then

$$\sum_{i=1}^m k_{ij}^d = \sum_{i=1}^m q_{ij}^d N_i.$$

Hence, if all group sizes are scaled by the same factor, this total scales by the same factor — demonstrating density dependence.

4.4 Results

In this section we present theoretical results on the qualitative sensitivity of the basic reproduction number R_0 and the final size to changes in demography, across several demography-dependent contact patterns. Our main result is that, under *domination (bilateral) contact patterns* — used here as a proxy for contact changes induced by ageing — an increase in the number of aged individuals decreases outbreak severity, measured by both R_0 and the fractional final size. Before turning to this, we present general theorems on properties and differentiability of R_0 and $1 - \sigma$. All proofs are given in Section 4.5.

4.4.1 Differentiability and R_0 -threshold property

We begin with stating a canonical property of R_0 (see Definition 4.2.6), stating that an outbreak occurs, if and only if $R_0 > 1$.

Theorem 4.4.1. *Under Assumption 4.2.4, consider (4.1). If and only if $R_0 > 1$, the final size equations (4.4) have a solution in $(0, 1)^m$. If so, this solution is unique.*

The next result shows the intuitive fact that, at the end of an outbreak, the average number of new infections caused by a single infectious individual is strictly less than one. To make this precise, we first define the next generation matrix *at time t* as

$$\mathbf{M}_t = \begin{pmatrix} \frac{S_1(t)}{N_1} \frac{p_{11} k_{11}(\mathbf{N})}{\alpha_1} & \cdots & \frac{S_1(t)}{N_1} \frac{p_{1m} k_{1m}(\mathbf{N})}{\alpha_m} \\ \vdots & \ddots & \vdots \\ \frac{S_m(t)}{N_m} \frac{p_{m1} k_{m1}(\mathbf{N})}{\alpha_1} & \cdots & \frac{S_m(t)}{N_m} \frac{p_{mm} k_{mm}(\mathbf{N})}{\alpha_m} \end{pmatrix}, \quad (4.19)$$

so that $R_0 = \lim_{t \downarrow -\infty} \rho(\mathbf{M}_t)$. We also write $\mathbf{M}_\infty := \lim_{t \rightarrow \infty} \mathbf{M}_t$.

Lemma 4.4.2. *Under Assumption 4.2.4, consider (4.1). If $R_0 > 1$, then $\rho(\mathbf{M}_\infty) < 1$.*

The results below establish differentiability properties of the outbreak severity measures R_0 and σ , which we will need in the following subsection. we first introduce several conventions regarding vector notations in this chapter.

Notation 4.4.3. Unless specified otherwise, all vectors are column vectors and are written in boldface. For $\mathbf{x}, \mathbf{y} \in \mathbb{R}^m$, $\mathbf{x} \geq \mathbf{y}$ means $x_i \geq y_i$ for every i ; $\mathbf{x} > \mathbf{y}$ means $\mathbf{x} \geq \mathbf{y}$ and $\mathbf{x} \neq \mathbf{y}$; and $\mathbf{x} \gg \mathbf{y}$ means $x_i > y_i$ for all i . The m -dimensional all-ones and zero vectors are denoted by $\mathbf{1}$ and $\mathbf{0}$, respectively. We use equivalent notations for matrices.

The following theorem establishes continuous differentiability for the vector σ . The proof, as provided in Section 4.5, uses the Implicit Function Theorem and relies mainly on Lemma 4.4.2.

Theorem 4.4.4. *Let $\tilde{N} \gg 0$, $\tilde{P} \gg 0$, and $\tilde{\alpha} \gg 0$. Assume:*

- (i) *the map $(N, P, \alpha) \mapsto M(N, P, \alpha)$ is continuously differentiable in an open neighbourhood of $(\tilde{N}, \tilde{P}, \tilde{\alpha})$;*
- (ii) *$M(\tilde{N}, \tilde{P}, \tilde{\alpha})$ is irreducible;*
- (iii) *$R_0(\tilde{N}, \tilde{P}, \tilde{\alpha}) = \rho(M(\tilde{N}, \tilde{P}, \tilde{\alpha})) > 1$.*

Then the non-trivial solution $\sigma \in (0, 1)^m$ of (4.4) is well defined and is continuously differentiable as a function of (N, P, α) in an open neighbourhood of $(\tilde{N}, \tilde{P}, \tilde{\alpha})$.

Lemma 4.4.5. *Let $\tilde{N} \gg 0$, $\tilde{P} \gg 0$, and $\tilde{\alpha} \gg 0$, and fix $i \in \{1, \dots, m\}$. Assume:*

- (i) *the map $x_i \mapsto K(x)$, with $x_j = \tilde{N}_j$ for $j \neq i$, is continuously differentiable in an open neighbourhood of $x_i = \tilde{N}_i$;*
- (ii) *$M(\tilde{N}, \tilde{P}, \tilde{\alpha})$ is irreducible.*

Then $R_0(N, \tilde{P}, \tilde{\alpha}) = \rho(M(N, \tilde{P}, \tilde{\alpha}))$, with $N_j = \tilde{N}_j$ for $j \neq i$, is continuously differentiable as a function of N_i in an open neighbourhood of $\tilde{N}_i$. Moreover, let $x^ \gg 0$ and $x \gg 0$ be the left and right eigenvectors of $M(\tilde{N}, \tilde{P}, \tilde{\alpha})$ corresponding to $R_0(\tilde{N}, \tilde{P}, \tilde{\alpha})$, normalised such that $(x^*)^\top x = 1$. Then*

$$\left. \frac{d R_0(N, \tilde{P}, \tilde{\alpha})}{d N_i} \right|_{N_i = \tilde{N}_i} = (x^*)^\top M'(\tilde{N}) x,$$

where $M'(\tilde{N})$ denotes the matrix obtained by differentiating $M(N, \tilde{P}, \tilde{\alpha})$ componentwise with respect to N_i and evaluating at $N = \tilde{N}$ (with $P = \tilde{P}$ and $\alpha = \tilde{\alpha}$ held fixed).

4.4.2 Results: frequency dependence

In this subsection we present several sensitivity results for demography-dependent contact patterns that are *frequency dependent*. By definition, frequency dependent patterns do not depend on the total population size N . Consequently, scaling N while keeping the composition $\mathbf{n}$ fixed leaves the transmission dynamics — and hence R_0 and the fractional final size — unchanged. We therefore focus on composition changes: changing the size of selected groups while holding others fixed. Specifically, we discuss bilateral contact patterns and power contact patterns; the results for bilateral contact patterns, interpreted as a proxy for demographic ageing, shed light on the ageing question as posed in the introduction.

Linear bilateral contact patterns

Theorem 4.4.6. *Consider (4.1) with a linear bilateral contact pattern $\mathbf{K}^b$. Let $\mathbf{N} \gg \mathbf{0}$ be such that $\mathbf{K}^b$ is irreducible and $R_0 = \rho(\mathbf{M}(\mathbf{N})) > 1$. Assume the population has a royal group z . Then*

$$\frac{dR_0}{dN_z} > 0 \quad \text{and} \quad \frac{d\sigma_i}{dN_z} < 0, \quad 1 \leq i \leq m.$$

Theorem 4.4.6 has a natural interpretation via the definition of a royal group. Recall that an individual from the royal group z has a fixed number of contacts k_{iz}^b with type- i individuals, independent of composition $\mathbf{n}$ and population size N . At any time t we reason as follows. As N_z increases, each non- z individual makes more contacts per unit time with z (since k_{zi}^b increases with N_z), so the force of infection experienced by group $i \neq z$ increases. Consequently — noting that contact rates between non-royal groups are unchanged — the fraction of susceptibles remaining in the non-royal groups must decrease, i.e., $d\sigma_i/dN_z < 0$ for $i \neq z$. Although the contact rate of royal individuals with each other does not change (see (4.16)), the higher number of infections in the other groups spills over to z , so we also expect $d\sigma_z/dN_z < 0$. The same line of reasoning leads us to conclude that $\frac{dR_0}{dN_z} > 0$ should hold as well. By symmetry, the converse holds for a servant group, as confirmed by the next theorem.

Theorem 4.4.7. *Consider (4.1) with a linear bilateral contact pattern $\mathbf{K}^b$. Let $\mathbf{N} \gg \mathbf{0}$ be such that $\mathbf{K}^b$ is irreducible and $R_0 = \rho(\mathbf{M}(\mathbf{N})) > 1$. Assume the population has a servant group z . Then*

$$\frac{dR_0}{dN_z} < 0 \quad \text{and} \quad \frac{d\sigma_i}{dN_z} > 0, \quad 1 \leq i \leq m.$$

On the ageing question. The above results can be interpreted in the context of population ageing and thus shed light on the ageing question posed in the introduction. Partition the population into three groups: young, middle-aged, and aged individuals. Young individuals can be informally viewed as a royal group, since each young person typically requires regular contacts with several caregivers and, in due course, with classmates. By contrast, aged individuals can be loosely interpreted as a servant group, reflecting that they often have fewer routine interactions. Under this heuristic assumption, a corollary of Theorem 4.4.7 is that an epidemic outbreak becomes less severe when the size of the aged group increases (i.e., under demographic ageing). More broadly, Theorems 4.4.6 and 4.4.7 show that, when assessing how a change in a group's size affects the basic reproduction number and the fractional final size, a central consideration is which contact rates are held fixed: the contact rate per unit time of each individual in the changing group (independent of composition) or, alternatively, the contact rates of individuals in the other groups.

Power contact patterns

As noted in Section 4.3.1, the demography-dependent power contact pattern is interesting from a mathematical point of view. In particular, in models with this pattern the basic reproduction number is independent of both composition and total size.

Theorem 4.4.8. *Consider (4.1) with a power contact pattern $\mathbf{K}^p$ with exponent $d \in \mathbb{R}$, and suppose $\mathbf{K}^p$ is irreducible for $N \gg 0$. Then R_0 is independent of N , i.e., it does not depend on the size or the composition of the population.*

The next statement follows immediately by substituting $d = 1$ into the final size equations (4.4).

Theorem 4.4.9. *Consider (4.1) with a power contact pattern $\mathbf{K}^p$ with $d = 1$, and suppose $\mathbf{K}^p$ is irreducible for $N \gg 0$. Then the fractional final size is independent of N , i.e., it does not depend on the size or the composition of the population.*

4.4.3 Results: density dependence

First, we present the main results for the linear density dependent contact patterns before discussing them.

Theorem 4.4.10. *Consider (4.1) with a linear density dependent contact pattern $\mathbf{K}^d$ that is irreducible for $N \gg 0$. Then, for every $z \in \{1, \dots, m\}$,*

$$\frac{dR_0}{dN_z} > 0.$$

For the next theorem, recall the notation, as introduced in Definition 4.2.6 in the context of the next generation matrix,

$$m_{ij} := \frac{p_{ij} k_{ij}^d}{\alpha_j},$$

which is the expected number of new infections generated in group i by a single infectious individual of type j during its infectious period in the earliest phase of the epidemic.

Theorem 4.4.11. *Consider (4.1) with a linear density dependent contact pattern $\mathbf{K}^d$ that is irreducible for $N \gg 0$. If $R_0 > 1$, then*

$$\frac{d\sigma_i}{dN_z} < 0, \quad \text{for } i, z \in \{1, \dots, m\}.$$

If, in addition, $m_{zz} > 1$, then also

$$\frac{dS_z(\infty)}{dN_z} < 0.$$

In contrast to frequency dependence, under density dependence the contact pattern — and hence the transmission dynamics — depends on both the composition and the population size. Clearly, if the population size N increases while the composition $\mathbf{n}$ remains fixed, all group sizes scale proportionally and the monotonicity results of Theorems 4.4.10 and 4.4.11 still apply. Moreover, Theorem 4.4.10 aligns with the intuition under the fixed pool metaphor: adding individuals increases contacts per unit time and thus increases the average number of infections caused by a single infectious individual at the earliest phase of an epidemic.

However, the effect of a composition change *only* (varying $\mathbf{n}$ at fixed N) on the basic reproduction number cannot be guessed from Theorem 4.4.10. To illustrate this, set

$$\tilde{m}_{ij} := \frac{p_{ij} q_{ij}^d}{\alpha_j} N, \quad i, j \in \{1, \dots, m\}. \quad (4.20)$$

With linear density dependence the next generation matrix can then be written as

$$\mathbf{M}(\mathbf{N}) = \begin{pmatrix} \tilde{m}_{11} n_1 & \cdots & \tilde{m}_{1m} n_1 \\ \vdots & \ddots & \vdots \\ \tilde{m}_{m1} n_m & \cdots & \tilde{m}_{mm} n_m \end{pmatrix}. \quad (4.21)$$

It is tempting to apply Lemma 4.4.5 to compute $\frac{dR_0}{dn_z}$, but a complicating factor is that one must satisfy the constraint $\sum_j n_j = 1$: a perturbation in n_z must be balanced by changes in other components. Thus, for $m > 2$ one must specify how the remaining n_i adjust when n_z changes. In the two-type case ($m = 2$), we obtain the following.

Theorem 4.4.12. *Consider the two-type ($m = 2$) model (4.1) with fixed population size N and a density dependent contact pattern such that $\mathbf{K}^d \gg \mathbf{0}$. Assume $\mathbf{P} \gg \mathbf{0}$. Then R_0 is a differentiable function of n_1 on $[0, 1]$, with at most one extremum. Moreover, the sign of the slope of R_0 at $n_1 = 0$, $n_1 = \frac{1}{2}$, and $n_1 = 1$ equals the sign of, respectively, $\tilde{m}_{12}\tilde{m}_{21} - \tilde{m}_{22}^2$, $\tilde{m}_{11} - \tilde{m}_{22}$, and $\tilde{m}_{11}^2 - \tilde{m}_{12}\tilde{m}_{21}$.*

Theorem 4.4.12 shows that the qualitative behaviour of R_0 as a function of the composition (here, of n_1) depends only on $(\tilde{m}_{ij})_{1 \leq i, j \leq 2}$ and, importantly, in contrast to the population size case of Theorem 4.4.10, need not be monotone in n_1 .

4.5 Proofs

In this section we provide, for each result in Section 4.4, its corresponding proof. We would like to pay special attention to the ideas developed by Schmidt [139], a PhD thesis from 1990, which inspired and shaped the proof strategies used for our main results.

Proof of Theorem 4.4.1 We follow the steps of the proof of a more general fixed-point result in Appendix B of Rass & Radcliffe [135]. Define, for each type i ,

$$\nu_i := 1 - \sigma_i \in [0, 1], \quad c_{ij} := \frac{\beta_{ij} N_j}{\alpha_j N_i}, \quad \mathbf{C} := (c_{ij})_{1 \leq i, j \leq m}.$$

Then $\sigma_j - 1 = -\nu_j$, so the final size equations (4.4) are equivalent to

$$\nu_i = 1 - \exp\left(-\sum_{j=1}^m c_{ij} \nu_j\right), \quad i = 1, \dots, m.$$

Thus $\boldsymbol{\nu} := (\nu_1, \dots, \nu_m)^\top$ is a solution to (4.35) (Theorem 4.A.2) in the Appendix, with $\mathbf{A} = \mathbf{C}$. Next, let $\boldsymbol{\Delta} := \text{diag}(\mathbf{N})$. By a direct calculation, $\mathbf{C} = \boldsymbol{\Delta}^{-1} \mathbf{M}(\mathbf{N}) \boldsymbol{\Delta}$, so $\mathbf{C}$ and the next generation matrix $\mathbf{M}(\mathbf{N})$ are similar and therefore have the same dominant eigenvalue: $\rho(\mathbf{C}) = \rho(\mathbf{M}(\mathbf{N})) = R_0$. Moreover, under Assumption 4.2.4 (and with $p_{ij} > 0$ whenever $k_{ij}(\mathbf{N}) > 0$), the matrix $\mathbf{C}$ is irreducible, so Theorem 4.A.2 in the Appendix applies directly, proving the desired. $\square$

Proof of Lemma 4.4.2 Assume $R_0 > 1$. We adapt the notation in the proof of Theorem 4.A.2. Now apply Lemma 4.A.3 (see Appendix) to $\mathbf{A} = \mathbf{C}$ and the fixed point $\mathbf{x} = \boldsymbol{\nu}$. It gives us that the matrix $\tilde{\mathbf{C}}$ with entries

$$\tilde{c}_{ij} = (1 - \nu_i)c_{ij} = \sigma_i c_{ij}$$

satisfies $\rho(\tilde{\mathbf{C}}) < 1$. Writing $\boldsymbol{\Sigma} := \text{diag}(\boldsymbol{\sigma})$, we have $\tilde{\mathbf{C}} = \boldsymbol{\Sigma}\mathbf{C}$ and thus $\rho(\boldsymbol{\Sigma}\mathbf{C}) < 1$. On the other hand, noting that $S_i(\infty) = \sigma_i N_i$ we have

$$(\mathbf{M}_\infty)_{ij} = \frac{S_i(\infty)}{N_i} \frac{p_{ij}k_{ij}(\mathbf{N})}{\alpha_j} = \sigma_i \frac{\beta_{ij}}{\alpha_j},$$

hence, $\mathbf{M}_\infty = \boldsymbol{\Sigma}\mathbf{M}(\mathbf{N})$. Now, using $\mathbf{C} = \boldsymbol{\Delta}^{-1}\mathbf{M}(\mathbf{N})\boldsymbol{\Delta}$, we compute

$$\boldsymbol{\Delta}(\boldsymbol{\Sigma}\mathbf{C})\boldsymbol{\Delta}^{-1} = \boldsymbol{\Delta}\boldsymbol{\Sigma}\boldsymbol{\Delta}^{-1}\mathbf{M}(\mathbf{N}) = \boldsymbol{\Sigma}\mathbf{M}(\mathbf{N}) = \mathbf{M}_\infty,$$

where we used that $\boldsymbol{\Delta}\boldsymbol{\Sigma}\boldsymbol{\Delta}^{-1} = \boldsymbol{\Sigma}$ since all three are diagonal. Hence $\mathbf{M}_\infty$ and $\boldsymbol{\Sigma}\mathbf{C}$ are similar. We conclude

$$\rho(\mathbf{M}_\infty) = \rho(\boldsymbol{\Sigma}\mathbf{C}) < 1,$$

as claimed. $\square$

Proof of Theorem 4.4.4 We prove the claim using the Implicit Function Theorem, where we show that the Jacobian matrix of the function under consideration is invertible. Define the vector-valued function $\mathbf{F} = (F_1, \dots, F_m)^\top$ by

$$F_i(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}, \mathbf{s}) := s_i - N_i \exp\left(\frac{1}{N_i} \sum_{j=1}^m \frac{p_{ij}k_{ij}(\mathbf{N})}{\alpha_j} (s_j - N_j)\right), \quad i = 1, \dots, m,$$

for $\mathbf{N} \gg \mathbf{0}$, $\mathbf{P} \gg \mathbf{0}$, $\boldsymbol{\alpha} \gg \mathbf{0}$, and $\mathbf{s} \in \mathbb{R}^m$. Note that $\mathbf{F}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}, \mathbf{s}) = \mathbf{0}$ is equivalent to the final size equations (4.4) after setting $s_i = S_i(\infty) = \sigma_i N_i$ and noting again that $\beta_{ij} = p_{ij}k_{ij}(\mathbf{N})$.

By assumption (i), the map $(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}) \mapsto \mathbf{M}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha})$ is continuously differentiable near $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$. Since the entries of $\mathbf{M}$ are $(\mathbf{M}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}))_{ij} = p_{ij}k_{ij}(\mathbf{N})/\alpha_j$, it follows that each F_i is continuously differentiable with respect to $(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}, \mathbf{s})$ in a neighbourhood of $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}, \mathbf{s})$ with $\tilde{\mathbf{N}} \gg \mathbf{0}$ (so the factors $1/N_i$ are smooth).

Next, by assumptions (ii) and (iii), $\mathbf{M}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$ is irreducible and $R_0(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) > 1$. Hence, by Theorem 4.4.1, the final size equations have a unique solution $\tilde{\boldsymbol{\sigma}} \in (0, 1)^m$. Define

$$\tilde{\mathbf{s}} := \text{diag}(\tilde{\mathbf{N}}) \tilde{\boldsymbol{\sigma}},$$

hence, by design, we have $\mathbf{F}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}, \tilde{\mathbf{s}}) = \mathbf{0}$.

We now compute the Jacobian of $\mathbf{F}$ with respect to $\mathbf{s}$. Fix $i, j \in \{1, \dots, m\}$. Differentiating F_i with respect to s_j gives

$$\frac{\partial F_i}{\partial s_j}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}, \mathbf{s}) = \delta_{ij} - N_i \exp\left(\frac{1}{N_i} \sum_{k=1}^m \frac{p_{ik}k_{ik}(\mathbf{N})}{\alpha_k} (s_k - N_k)\right) \cdot \frac{1}{N_i} \frac{p_{ij}k_{ij}(\mathbf{N})}{\alpha_j},$$

where $\delta_{ij} = 1$ if $i = j$ and 0 otherwise. Evaluating at $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}, \tilde{\mathbf{s}})$ and using that

$$\tilde{s}_i = \tilde{N}_i \exp \left(\frac{1}{\tilde{N}_i} \sum_{k=1}^m \frac{\tilde{p}_{ik} k_{ik}(\tilde{\mathbf{N}})}{\tilde{\alpha}_k} (\tilde{s}_k - \tilde{N}_k) \right),$$

we obtain

$$\left. \frac{\partial F_i}{\partial s_j} \right|_{(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}, \tilde{\mathbf{s}})} = \delta_{ij} - \tilde{\sigma}_i \frac{\tilde{p}_{ij} k_{ij}(\tilde{\mathbf{N}})}{\tilde{\alpha}_j}.$$

In matrix form, the Jacobian matrix becomes

$$\left(\frac{\partial F_i}{\partial s_j} \right)_{1 \leq i, j \leq m} \bigg|_{(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}, \tilde{\mathbf{s}})} = \mathbf{I} - \mathbf{M}_\infty,$$

because $(\mathbf{M}_\infty)_{ij} = \frac{S_i(\infty)}{N_i} \frac{p_{ij} k_{ij}(\mathbf{N})}{\alpha_j} = \sigma_i \frac{p_{ij} k_{ij}(\mathbf{N})}{\alpha_j}$ by definition of $\mathbf{M}_t$.

By Lemma 4.4.2, $\rho(\mathbf{M}_\infty) < 1$. Hence every eigenvalue λ of $\mathbf{M}_\infty$ satisfies $|\lambda| < 1$, so 1 is not an eigenvalue of $\mathbf{M}_\infty$. Importantly, $\det(\mathbf{I} - \mathbf{M}_\infty) \neq 0$, and therefore the Jacobian matrix at $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}, \tilde{\mathbf{s}})$ is invertible.

We can now apply the Implicit Function Theorem: there exists an open neighbourhood U of $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$ and a unique *continuously differentiable* map $(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}) \mapsto \mathbf{s}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha})$ defined on U such that $\mathbf{s}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) = \tilde{\mathbf{s}}$ and $\mathbf{F}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}, \mathbf{s}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha})) = \mathbf{0}$ for all $(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}) \in U$. In other words, $\mathbf{s}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}) = \mathbf{S}(\infty)$ varies smoothly with $(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha})$ near $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$.

Finally, $\boldsymbol{\sigma}$ is obtained componentwise by $\sigma_i = s_i/N_i$, i.e.

$$\boldsymbol{\sigma}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}) = \text{diag}(\mathbf{N})^{-1} \mathbf{s}(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha}).$$

Since $\mathbf{N} \gg \mathbf{0}$ on U , the map $\mathbf{N} \mapsto \text{diag}(\mathbf{N})^{-1}$ is smooth, and thus $\boldsymbol{\sigma}$ is continuously differentiable as a function of $(\mathbf{N}, \mathbf{P}, \boldsymbol{\alpha})$ on a neighbourhood of $(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$. $\square$

Proof of Lemma 4.4.5 Fix $i \in \{1, \dots, m\}$ and vary N_i while keeping $N_j = \tilde{N}_j$ for $j \neq i$, and $\mathbf{P} = \tilde{\mathbf{P}}, \boldsymbol{\alpha} = \tilde{\boldsymbol{\alpha}}$ fixed. By definition,

$$\mathbf{M}(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) = \left(\frac{\tilde{p}_{ij} k_{ij}(\mathbf{N})}{\tilde{\alpha}_j} \right)_{1 \leq i, j \leq m}.$$

Assumption (i) implies that $N_i \mapsto k_{ij}(\mathbf{N})$ is continuously differentiable near $N_i = \tilde{N}_i$ for each j , hence $N_i \mapsto \mathbf{M}(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$ is element-wise continuously differentiable near $N_i = \tilde{N}_i$.

By assumption (ii), the matrix $\mathbf{M}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$ is irreducible. Hence its dominant eigenvalue $R_0(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})$ has multiplicity one and admits strictly positive left and right eigenvectors. Standard perturbation theory such as Lax [98] or Caswell [30] implies that $R_0(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) = \rho(\mathbf{M}(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}))$ is continuously differentiable as a function of N_i in a neighbourhood of $\tilde{N}_i$.

Now, choose associated left and right eigenvectors $\mathbf{x}^*(N_i) \gg \mathbf{0}$ and $\mathbf{x}(N_i) \gg \mathbf{0}$ such that

$$(\mathbf{x}^*(N_i))^\top \mathbf{x}(N_i) = 1 \quad \text{for } N_i \text{ near } \tilde{N}_i.$$

In particular, $\mathbf{x}^* := \mathbf{x}^*(\tilde{N}_i)$ and $\mathbf{x} := \mathbf{x}(\tilde{N}_i)$ satisfy

$$\mathbf{M}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) \mathbf{x} = R_0(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) \mathbf{x}, \quad (\mathbf{x}^*)^\top \mathbf{M}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) = R_0(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) (\mathbf{x}^*)^\top,$$

and $(\mathbf{x}^*)^\top \mathbf{x} = 1$.

Differentiating the eigenvalue equation $\mathbf{M}(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) \mathbf{x}(N_i) = R_0(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) \mathbf{x}(N_i)$ with respect to N_i and evaluate at $N_i = \tilde{N}_i$, and writing

$$\mathbf{M}'(\tilde{\mathbf{N}}) := \left. \frac{d \mathbf{M}(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})}{dN_i} \right|_{N_i=\tilde{N}_i}, \quad \mathbf{x}' := \left. \frac{d \mathbf{x}(N_i)}{dN_i} \right|_{N_i=\tilde{N}_i}, \quad R'_0 := \left. \frac{d R_0(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})}{dN_i} \right|_{N_i=\tilde{N}_i},$$

we obtain

$$\mathbf{M}'(\tilde{\mathbf{N}}) \mathbf{x} + \mathbf{M}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) \mathbf{x}' = R'_0 \mathbf{x} + R_0(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) \mathbf{x}'.$$

Left-multiplying by $(\mathbf{x}^*)^\top$ and using $(\mathbf{x}^*)^\top \mathbf{M}(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) = R_0(\tilde{\mathbf{N}}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}}) (\mathbf{x}^*)^\top$, the terms involving $\mathbf{x}'$ cancel, yielding

$$(\mathbf{x}^*)^\top \mathbf{M}'(\tilde{\mathbf{N}}) \mathbf{x} = R'_0 (\mathbf{x}^*)^\top \mathbf{x}.$$

Finally, $(\mathbf{x}^*)^\top \mathbf{x} = 1$ gives

$$\left. \frac{d R_0(\mathbf{N}, \tilde{\mathbf{P}}, \tilde{\boldsymbol{\alpha}})}{dN_i} \right|_{N_i=\tilde{N}_i} = (\mathbf{x}^*)^\top \mathbf{M}'(\tilde{\mathbf{N}}) \mathbf{x},$$

as claimed. $\square$

Proof of Theorem 4.4.6 Recall that under a linear bilateral contact pattern (4.16),

$$k_{ij}^b(\mathbf{N}) = q_{ij} \frac{N_i}{c_{ij}N_i + (1 - c_{ij})N_j}, \quad 1 \leq i, j \leq m,$$

so the next generation matrix $\mathbf{M}(\mathbf{N})$ has entries

$$(\mathbf{M}(\mathbf{N}))_{ij} = \frac{p_{ij} k_{ij}^b(\mathbf{N})}{\alpha_j} = u_{ij} \frac{N_i}{c_{ij}N_i + (1 - c_{ij})N_j}, \quad u_{ij} := \frac{p_{ij} q_{ij}}{\alpha_j}.$$

This proof consists of two steps. In Step 1 we prove the sign of dR_0/dN_z , in Step 2 we do the same for $d\sigma_i/dN_z$. Let us start with Step 1.

◦ *Step 1: the sign of dR_0/dN_z .* Because $N_z \mapsto \mathbf{K}^b(\mathbf{N})$ is continuously differentiable, the same holds for $N_z \mapsto \mathbf{M}(\mathbf{N})$. Since $\mathbf{K}^b$ is irreducible and $\mathbf{P} \gg \mathbf{0}$, the matrix $\mathbf{M}(\mathbf{N})$ is irreducible, hence, by Lemma 4.4.5,

$$\frac{dR_0}{dN_z} = \mathbf{v}^{*\top} \mathbf{M}'(\mathbf{N}) \mathbf{v},$$

where $\mathbf{M}'(\mathbf{N})$ denotes the matrix obtained by differentiating $\mathbf{M}(\mathbf{N})$ componentwise with respect to N_z and $\mathbf{v}^* \gg \mathbf{0}$ and $\mathbf{v} \gg \mathbf{0}$ the left and right eigenvectors corresponding to R_0 , with the normalization $\mathbf{v}^{*\top} \mathbf{v} = 1$.

Note first that $(\mathbf{M}(\mathbf{N}))_{ii} = u_{ii}$ for any i , hence independent of N_z . Now use that z is a royal group. By definition, this means $c_{iz} = 1$ for all $i \neq z$. In particular, for every $i \neq z$,

$$(\mathbf{M}(\mathbf{N}))_{iz} = u_{iz} \frac{N_i}{c_{iz}N_i + (1 - c_{iz})N_z} = u_{iz} \frac{N_i}{N_i} = u_{iz},$$

so the z th column does not depend on N_z , representing that an individual of a royal group does not adjust its contact rate as a result of change in group sizes. Moreover, for $j \neq z$ we have $c_{zj} = 0$ (since $c_{zj} = 1 - c_{jz}$ in a domination pair, see Case 1 of Section 4.3.1), and hence

$$(\mathbf{M}(\mathbf{N}))_{zj} = u_{zj} \frac{N_z}{c_{zj}N_z + (1 - c_{zj})N_j} = u_{zj} \frac{N_z}{N_j},$$

which depends linearly on N_z . Therefore $\mathbf{M}'(\mathbf{N})$ has zeros everywhere except in the z th row, and for $j \neq z$,

$$(\mathbf{M}'(\mathbf{N}))_{zj} = \frac{u_{zj}}{N_j} > 0.$$

Consequently,

$$\frac{dR_0}{dN_z} = \sum_{j=1}^m v_z^* (\mathbf{M}'(\mathbf{N}))_{zj} v_j = \sum_{j \neq z} v_z^* \frac{u_{zj}}{N_j} v_j > 0,$$

because $v_z^* > 0$, $u_{zj} > 0$, $N_j > 0$, and $v_j > 0$.

◦ *Step 2: the sign of $d\sigma_i/dN_z$.* Since $R_0 > 1$ and $\mathbf{M}(\mathbf{N})$ is irreducible, Theorem 4.4.1 gives a unique solution $\boldsymbol{\sigma} \in (0, 1)^m$ of the final size equations, and Theorem 4.4.4 implies that each σ_i is differentiable with respect to N_z . Define the derivative vector

$$\mathbf{D}_z := \left(\frac{d\sigma_1}{dN_z}, \dots, \frac{d\sigma_m}{dN_z} \right)^\top.$$

Write the final size equations (4.4) in the form

$$\sigma_i = \exp \left(\sum_{j=1}^m u_{ij} \frac{N_j}{c_{ij}N_i + (1 - c_{ij})N_j} (\sigma_j - 1) \right), \quad i = 1, \dots, m.$$

Differentiate both sides with respect to N_z . For $i \neq z$, the only coefficient that depends on N_z is the one with $j = z$. Using $c_{iz} = 1$ we have

$$u_{iz} \frac{N_z}{c_{iz}N_i + (1 - c_{iz})N_z} = u_{iz} \frac{N_z}{N_i}, \quad \text{so} \quad \frac{d}{dN_z} \left(u_{iz} \frac{N_z}{N_i} \right) = \frac{u_{iz}}{N_i}.$$

Applying the chain rule therefore yields, for $i \neq z$,

$$\frac{d\sigma_i}{dN_z} = \sigma_i \left[\sum_{j=1}^m u_{ij} \frac{N_j}{c_{ij}N_i + (1 - c_{ij})N_j} \frac{d\sigma_j}{dN_z} + \frac{u_{iz}}{N_i} (\sigma_z - 1) \right]. \quad (4.22)$$

For $i = z$, note that for $j \neq z$ we have $c_{zj} = 0$, so $u_{zj} \frac{N_j}{c_{zj}N_z + (1 - c_{zj})N_j} = u_{zj}$, which is independent of N_z , and the $j = z$ term is also independent of N_z . Hence there is no ‘extra’ derivative term, and we obtain

$$\frac{d\sigma_z}{dN_z} = \sigma_z \left[\sum_{j=1}^m u_{zj} \frac{N_j}{c_{zj}N_z + (1 - c_{zj})N_j} \frac{d\sigma_j}{dN_z} \right]. \quad (4.23)$$

Next, introduce $\Delta = \text{diag}(\mathbf{N})$ and recall $\mathbf{M}_\infty = \text{diag}(\boldsymbol{\sigma}) \mathbf{M}(\mathbf{N})$. Define the similar matrix

$$\mathbf{M}_\infty^* := \Delta^{-1} \mathbf{M}_\infty \Delta.$$

A direct substitution shows that $\mathbf{M}_\infty^*$ has entries

$$(\mathbf{M}_\infty^*)_{ij} = \sigma_i u_{ij} \frac{N_j}{c_{ij} N_i + (1 - c_{ij}) N_j}.$$

Using (4.22)–(4.23) and rearranging terms gives us the main linear equation in this proof:

$$\mathbf{b}_z = (\mathbf{I} - \mathbf{M}_\infty^*) \mathbf{D}_z, \quad (4.24)$$

where $\mathbf{b}_z \in \mathbb{R}^m$ is defined componentwise by

$$(\mathbf{b}_z)_i = \begin{cases} \sigma_i \frac{u_{iz}}{N_i} (\sigma_z - 1), & i \neq z, \\ 0, & i = z. \end{cases}$$

Since $\boldsymbol{\sigma} \in (0, 1)^m$, we have $\sigma_z - 1 < 0$, and thus $\mathbf{b}_z \leq \mathbf{0}$. Moreover, $\mathbf{M}(\mathbf{N})$ is irreducible, so in particular $u_{iz} > 0$ for some $i \neq z$; hence $\mathbf{b}_z$ has at least one strictly negative component.

By Lemma 4.4.2, $\rho(\mathbf{M}_\infty) < 1$. Because $\mathbf{M}_\infty^*$ is similar to $\mathbf{M}_\infty$, it has the same eigenvalues and thus $\rho(\mathbf{M}_\infty^*) < 1$ as well. Therefore $\mathbf{I} - \mathbf{M}_\infty^*$ is invertible and we have that matrix geometric series converges: $(\mathbf{I} - \mathbf{M}_\infty^*)^{-1} = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty^*)^\ell$, and hence:

$$\mathbf{D}_z = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty^*)^\ell \mathbf{b}_z.$$

Each power $(\mathbf{M}_\infty^*)^\ell$ is entrywise nonnegative, and $\mathbf{b}_z \leq \mathbf{0}$, so every term $(\mathbf{M}_\infty^*)^\ell \mathbf{b}_z \leq \mathbf{0}$. This already implies $\mathbf{D}_z \leq \mathbf{0}$.

To prove strict negativity in every component, pick an index $n \neq z$ such that $(\mathbf{b}_z)_n < 0$. The matrix $\mathbf{M}_\infty^*$ is irreducible (it has the same zero pattern as $\mathbf{M}(\mathbf{N})$, since $\boldsymbol{\sigma} \gg \mathbf{0}$ and Δ is diagonal). Hence, for each $i \in \{1, \dots, m\}$ there exists $\ell_i \geq 0$ such that $((\mathbf{M}_\infty^*)^{\ell_i})_{in} > 0$. Looking at the i th component of the series,

$$(\mathbf{D}_z)_i = \sum_{\ell=0}^{\infty} \sum_{j=1}^m ((\mathbf{M}_\infty^*)^\ell)_{ij} (\mathbf{b}_z)_j,$$

all summands are ≤ 0 , and the specific summand with $\ell = \ell_i$ and $j = n$ equals $((\mathbf{M}_\infty^*)^{\ell_i})_{in} (\mathbf{b}_z)_n < 0$. Therefore $(\mathbf{D}_z)_i < 0$ for every i , proving the desired: $d\sigma_i/dN_z < 0$ for all $1 \leq i \leq m$.

□

Proof of Theorem 4.4.7 We follow the proof of Theorem 4.4.6 and indicate only the changes that occur when z is a servant group.

Step 1: the sign of dR_0/dN_z . As in the proof of Theorem 3, differentiability of $N_z \mapsto \mathbf{K}^b(\mathbf{N})$ implies differentiability of $N_z \mapsto \mathbf{M}(\mathbf{N})$, and irreducibility yields strictly positive

left and right eigenvectors $\mathbf{v}^* \gg \mathbf{0}$ and $\mathbf{v} \gg \mathbf{0}$, normalised by $\mathbf{v}^{*\top} \mathbf{v} = 1$. Lemma 4.4.5 gives

$$\frac{dR_0}{dN_z} = \mathbf{v}^{*\top} \mathbf{M}'(\mathbf{N}) \mathbf{v}.$$

If z is a servant type, then $c_{iz} = 0$ for all $i \neq z$. Hence, for every $i \neq z$,

$$(\mathbf{M}(\mathbf{N}))_{iz} = u_{iz} \frac{N_i}{c_{iz}N_i + (1 - c_{iz})N_z} = u_{iz} \frac{N_i}{N_z},$$

so the dependence on N_z is now in the z th column (instead of the z th row in the proof of Theorem 4.4.6). In contrast, for $j \neq z$ we have $c_{zj} = 1$ and thus

$$(\mathbf{M}(\mathbf{N}))_{zj} = u_{zj} \frac{N_z}{c_{zj}N_z + (1 - c_{zj})N_j} = u_{zj},$$

which does not depend on N_z . Therefore $\mathbf{M}'(\mathbf{N})$ has zeros everywhere except possibly in the z th column, and for $i \neq z$,

$$(\mathbf{M}'(\mathbf{N}))_{iz} = -u_{iz} \frac{N_i}{N_z^2} < 0.$$

Consequently,

$$\frac{dR_0}{dN_z} = \sum_{i=1}^m \sum_{j=1}^m v_i^* (\mathbf{M}'(\mathbf{N}))_{ij} v_j = \sum_{i \neq z} v_i^* (\mathbf{M}'(\mathbf{N}))_{iz} v_z < 0,$$

since $v_i^* > 0$, $v_z > 0$, and $(\mathbf{M}'(\mathbf{N}))_{iz} < 0$ for all $i \neq z$.

Step 2: the sign of $d\sigma_i/dN_z$. As in Theorem 4.4.6, Theorem 4.4.4 implies that each σ_i is differentiable with respect to N_z . Let

$$\mathbf{D}_z := \left(\frac{d\sigma_1}{dN_z}, \dots, \frac{d\sigma_m}{dN_z} \right)^\top.$$

Differentiating the final size equations gives again a linear system of the form

$$\mathbf{b}_z = (\mathbf{I} - \mathbf{M}_\infty^*) \mathbf{D}_z,$$

where $\mathbf{M}_\infty^* = \mathbf{\Delta}^{-1} \mathbf{M}_\infty \mathbf{\Delta}$ with $\mathbf{\Delta} = \text{diag}(\mathbf{N})$, and $\mathbf{M}_\infty = \text{diag}(\boldsymbol{\sigma}) \mathbf{M}(\mathbf{N})$. The only difference from Theorem 3 is that, because z is a servant type, one finds that $\mathbf{b}_z \geq \mathbf{0}$ and that at least one component of $\mathbf{b}_z$ is strictly positive.

As in the proof of Theorem 3, Lemma 4.4.2 implies $\rho(\mathbf{M}_\infty) < 1$, hence also $\rho(\mathbf{M}_\infty^*) < 1$. Therefore

$$(\mathbf{I} - \mathbf{M}_\infty^*)^{-1} = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty^*)^\ell, \quad \text{and thus} \quad \mathbf{D}_z = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty^*)^\ell \mathbf{b}_z.$$

By the same irreducibility-argument as in the proof of Theorem 4.4.6 we obtain that $(\mathbf{D}_z)_i > 0$, and, hence $d\sigma_i/dN_z > 0$ for all i . This completes the proof. $\square$

Proof of Theorem 4.4.8 Under the power contact pattern $\mathbf{K}^p(\mathbf{N})$, see (4.17), the contact rates satisfy

$$k_{ij}^p(\mathbf{N}) = q_{ij}^p \left(\frac{N_i}{N_j} \right)^d, \quad 1 \leq i, j \leq m,$$

with $q_{ij}^p = q_{ji}^p > 0$ and $d \in \mathbb{R}$. Therefore the next generation matrix $\mathbf{M}(\mathbf{N})$ has entries

$$(\mathbf{M}(\mathbf{N}))_{ij} = \frac{p_{ij} k_{ij}^p(\mathbf{N})}{\alpha_j} = \frac{p_{ij} q_{ij}^p}{\alpha_j} \left(\frac{N_i}{N_j} \right)^d = u_{ij} N_i^d N_j^{-d},$$

where we introduce the $\mathbf{N}$ -independent constants $u_{ij} := \frac{p_{ij} q_{ij}^p}{\alpha_j} > 0$. Write the matrix of these parameters as $\mathbf{U} := (u_{ij})_{1 \leq i, j \leq m}$.

Next define the diagonal matrix

$$\Delta_d := \text{diag}(N_1^d, \dots, N_m^d).$$

Since $\mathbf{N} \gg \mathbf{0}$, each $N_i^d > 0$ and hence Δ_d is invertible with $\Delta_d^{-1} = \text{diag}(N_1^{-d}, \dots, N_m^{-d})$. A direct componentwise calculation now shows that $\mathbf{M}(\mathbf{N})$ is similar to $\mathbf{U}$: $(\Delta_d \mathbf{U} \Delta_d^{-1})_{ij} = (\Delta_d)_{ii} u_{ij} (\Delta_d^{-1})_{jj} = N_i^d u_{ij} N_j^{-d} = (\mathbf{M}(\mathbf{N}))_{ij}$. Thus

$$\mathbf{M}(\mathbf{N}) = \Delta_d \mathbf{U} \Delta_d^{-1}.$$

Because similar matrices have the identical eigenvalues, we have

$$R_0(\mathbf{N}) = \rho(\mathbf{M}(\mathbf{N})) = \rho(\mathbf{U}),$$

which is independent of $\mathbf{N}$. Therefore R_0 does not depend on population size or composition. $\square$

Proof of Theorem 4.4.9 By plugging in $d = 1$ in the final size equations (4.4) with the power contact pattern (4.17) we find that the final size equations become independent of the population size N and the composition $\mathbf{n}$. $\square$

Proof of Theorem 4.4.10. The proof uses the same strategy as in the proof of Theorem 4.4.6: we combine the eigenvalue derivative formula from Lemma 4.4.5 with an explicit sign computation of the matrix derivative. The difference is that for linear density dependence the derivative has a particularly simple form.

Under a linear density dependent contact pattern, see (4.18),

$$k_{ij}^d(\mathbf{N}) = q_{ij}^d N_i, \quad 1 \leq i, j \leq m,$$

and hence the next generation matrix $\mathbf{M}(\mathbf{N})$ has entries

$$(\mathbf{M}(\mathbf{N}))_{ij} = \frac{p_{ij} k_{ij}^d(\mathbf{N})}{\alpha_j} = \frac{p_{ij} q_{ij}^d}{\alpha_j} N_i = u_{ij}^d N_i,$$

with $u_{ij}^d := \frac{p_{ij}q_{ij}^d}{\alpha_j} > 0$. Fix $z \in \{1, \dots, m\}$ and differentiate $\mathbf{M}(\mathbf{N})$ componentwise with respect to N_z , denote this matrix by $\mathbf{M}'(\mathbf{N})$. Since each entry depends linearly on N_i through the row index i , we obtain

$$\mathbf{M}'(\mathbf{N})_{ij} = \begin{cases} u_{zj}^d, & i = z, \\ 0, & i \neq z. \end{cases}$$

In particular, $\mathbf{M}'(\mathbf{N}) \geq \mathbf{0}$, and its z th row is strictly positive. Because $\mathbf{K}^d$ is irreducible for $\mathbf{N} \gg \mathbf{0}$, the matrix $\mathbf{M}(\mathbf{N})$ is irreducible with strictly positive entries for $\mathbf{N} \gg \mathbf{0}$. Let $\mathbf{x}^* \gg \mathbf{0}$ and $\mathbf{x} \gg \mathbf{0}$ be the left and right eigenvectors of $\mathbf{M}(\mathbf{N})$, normalised by $(\mathbf{x}^*)^\top \mathbf{x} = 1$. By Lemma 4.4.5,

$$\frac{dR_0}{dN_z} = (\mathbf{x}^*)^\top \mathbf{M}'(\mathbf{N}) \mathbf{x}.$$

Using the explicit form of $\mathbf{M}'(\mathbf{N})$, we compute $(\mathbf{x}^*)^\top \mathbf{M}'(\mathbf{N}) \mathbf{x} = \sum_{j=1}^m x_z^* u_{zj}^d x_j$. Here $x_z^* > 0$ and $x_j > 0$ for all j . Moreover, since $\mathbf{M}(\mathbf{N})$ is irreducible, the z th row cannot be identically zero, so there exists at least one index j with $u_{zj}^d > 0$. Therefore at least one summand is strictly positive and all summands are nonnegative, which implies $(\mathbf{x}^*)^\top \mathbf{M}'(\mathbf{N}) \mathbf{x} > 0$. Hence $dR_0/dN_z > 0$. $\square$

Proof of Theorem 4.4.11. The following proof follows primarily the logic as used in the proof of Theorem 4.4.6. Throughout, assume $R_0 > 1$. Then, by Theorem 4.4.1, the final size equations admit a unique solution $\boldsymbol{\sigma} \in (0, 1)^m$, and by Theorem 4.4.4 each σ_i is differentiable with respect to each group size N_z .

◦ *Step 1:* $\frac{d\sigma_i}{dN_z} < 0$ for all i, z . Under linear density dependence (4.18), $k_{ij}^d(\mathbf{N}) = q_{ij}^d N_i$, so $\beta_{ij} = p_{ij} q_{ij}^d N_i$. Introduce

$$u_{ij}^d := \frac{p_{ij} q_{ij}^d}{\alpha_j} \geq 0.$$

Then the coefficient in the final size equations (4.4) simplifies to $\frac{\beta_{ij}}{\alpha_j} \frac{N_j}{N_i} = \frac{p_{ij} q_{ij}^d N_i}{\alpha_j} \frac{N_j}{N_i} = u_{ij}^d N_j$, and hence the final size equations can be written as

$$\sigma_i = \exp \left(\sum_{j=1}^m u_{ij}^d N_j (\sigma_j - 1) \right), \quad i = 1, \dots, m. \quad (4.25)$$

Fix $z \in \{1, \dots, m\}$ and differentiate (4.25) with respect to N_z , keeping N_j fixed for $j \neq z$. We obtain, for each i ,

$$\frac{d\sigma_i}{dN_z} = \sigma_i \left[u_{iz}^d (\sigma_z - 1) + \sum_{j=1}^m u_{ij}^d N_j \frac{d\sigma_j}{dN_z} \right]. \quad (4.26)$$

Define, as in the proof of earlier theorems, the derivative vector

$$\mathbf{D}_z := \left(\frac{d\sigma_1}{dN_z}, \dots, \frac{d\sigma_m}{dN_z} \right)^\top,$$

and define the matrix $\mathbf{C} = (c_{ij})_{1 \leq i, j \leq m}$ by $c_{ij} := u_{ij}^d N_j$. Then (4.26) is equivalent to the linear system

$$(\mathbf{I} - \mathbf{M}_\infty^*) \mathbf{D}_z = \mathbf{b}_z, \quad (4.27)$$

where $\mathbf{M}_\infty^* := \text{diag}(\boldsymbol{\sigma}) \mathbf{C}$, and $(\mathbf{b}_z)_i := \sigma_i u_{iz}^d (\sigma_z - 1)$ for $i = 1, \dots, m$. This is the same step as in Step 2 of the proof of Theorem 4.4.6.

Since $\sigma_z \in (0, 1)$, we have $\sigma_z - 1 < 0$, and hence $\mathbf{b}_z \leq \mathbf{0}$. Moreover, because the contact pattern is irreducible for $\mathbf{N} \gg \mathbf{0}$ and $p_{ij} > 0$ whenever $k_{ij}(\mathbf{N}) > 0$, the matrix $\mathbf{M}(\mathbf{N})$ is irreducible and the z th column cannot be identically zero; therefore, there exists at least one index n such that $u_{nz}^d > 0$: $\mathbf{b}_z$ has at least one strictly negative component.

Next, we show that $\rho(\mathbf{M}_\infty^*) < 1$. For this, write as before $\boldsymbol{\Delta} = \text{diag}(\mathbf{N})$. A direct calculation shows that

$$\mathbf{C} = \boldsymbol{\Delta}^{-1} \mathbf{M}(\mathbf{N}) \boldsymbol{\Delta},$$

hence,

$$\mathbf{M}_\infty^* = \text{diag}(\boldsymbol{\sigma}) \mathbf{C} = \text{diag}(\boldsymbol{\sigma}) \boldsymbol{\Delta}^{-1} \mathbf{M}(\mathbf{N}) \boldsymbol{\Delta} = \boldsymbol{\Delta}^{-1} \text{diag}(\boldsymbol{\sigma}) \mathbf{M}(\mathbf{N}) \boldsymbol{\Delta} = \boldsymbol{\Delta}^{-1} \mathbf{M}_\infty \boldsymbol{\Delta},$$

where we used that diagonal matrices commute. Therefore $\mathbf{M}_\infty^*$ is similar to $\mathbf{M}_\infty$, so they share the same eigenvalues. Thus, by Lemma 4.4.2, $\rho(\mathbf{M}_\infty) < 1$, and therefore $\rho(\mathbf{M}_\infty^*) < 1$. Consequently $\mathbf{I} - \mathbf{M}_\infty^*$ is invertible and the matrix geometric series converges. Applying this to (4.27) gives

$$\mathbf{D}_z = (\mathbf{I} - \mathbf{M}_\infty^*)^{-1} \mathbf{b}_z = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty^*)^\ell \mathbf{b}_z \leq \mathbf{0}.$$

To obtain strict negativity in every component of $\mathbf{D}_z$, pick n such that $(\mathbf{b}_z)_n < 0$. The matrix $\mathbf{M}_\infty^*$ is irreducible, hence, for every $i \in \{1, \dots, m\}$ there exists $\ell_i \geq 0$ with $((\mathbf{M}_\infty^*)^{\ell_i})_{in} > 0$. Consider the i th component of the series:

$$(\mathbf{D}_z)_i = \sum_{\ell=0}^{\infty} \sum_{j=1}^m ((\mathbf{M}_\infty^*)^\ell)_{ij} (\mathbf{b}_z)_j.$$

All summands are ≤ 0 , and the specific summand with $\ell = \ell_i$ and $j = n$ equals $((\mathbf{M}_\infty^*)^{\ell_i})_{in} (\mathbf{b}_z)_n < 0$. Therefore $(\mathbf{D}_z)_i < 0$ for every i , i.e.

$$\frac{d\sigma_i}{dN_z} < 0, \quad i = 1, \dots, m,$$

proving the first claim.

◦ *Step 2: if $m_{zz} > 1$, then $\frac{dS_z(\infty)}{dN_z} < 0$.* Let $s_i := S_i(\infty) = \sigma_i N_i$ and $\mathbf{s} := (s_1, \dots, s_m)^\top$. Under linear density dependence, the final size equations can be written in terms of $\mathbf{s}$ as

$$s_i = N_i \exp \left(\frac{1}{N_i} \sum_{j=1}^m m_{ij} (s_j - N_j) \right), \quad i = 1, \dots, m, \quad (4.28)$$

because $\frac{p_{ij} k_{ij}^d}{\alpha_j} = m_{ij}$ by definition.

Fix z and differentiate (4.28) with respect to N_z . Write $\mathbf{s}'_z := \left(\frac{ds_1}{dN_z}, \dots, \frac{ds_m}{dN_z}\right)^\top$. For $i \neq z$, we obtain

$$\frac{ds_i}{dN_z} = s_i \left(\frac{1}{N_i} \sum_{j=1}^m m_{ij} \frac{ds_j}{dN_z} - \frac{m_{iz}}{N_i} \right).$$

For $i = z$, we have the prefactor N_z to be taken into account, which gives an additional term:

$$\frac{ds_z}{dN_z} = \sigma_z + s_z \left(\frac{1}{N_z} \sum_{j=1}^m m_{zj} \frac{ds_j}{dN_z} - \frac{m_{zz}}{N_z} \right).$$

Rearranging these identities for all i yields the linear system

$$(\mathbf{I} - \mathbf{M}_\infty) \mathbf{s}'_z = \mathbf{r}_z, \quad (4.29)$$

where $\mathbf{M}_\infty = \text{diag}(\boldsymbol{\sigma})\mathbf{M}(\mathbf{N})$ and

$$(\mathbf{r}_z)_i = \begin{cases} -s_i \frac{m_{iz}}{N_i}, & i \neq z, \\ \sigma_z - s_z \frac{m_{zz}}{N_z}, & i = z. \end{cases}$$

For $i \neq z$, we have $(\mathbf{r}_z)_i < 0$. For the z th component, note that $s_z = N_z \sigma_z$, so $(\mathbf{r}_z)_z = \sigma_z - s_z \frac{m_{zz}}{N_z} = \sigma_z - \sigma_z m_{zz} = \sigma_z(1 - m_{zz})$. Hence, since $m_{zz} > 1$ as assumed in the Theorem, we have $(\mathbf{r}_z)_z < 0$ and thus $\mathbf{r}_z \ll \mathbf{0}$.

Finally, Lemma 4.4.2 gives $\rho(\mathbf{M}_\infty) < 1$, so $\mathbf{I} - \mathbf{M}_\infty$ is invertible and $(\mathbf{I} - \mathbf{M}_\infty)^{-1} = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty)^\ell$, with each $(\mathbf{M}_\infty)^\ell$ entrywise nonnegative. Applying this to (4.29) yields

$$\mathbf{s}'_z = (\mathbf{I} - \mathbf{M}_\infty)^{-1} \mathbf{r}_z = \sum_{\ell=0}^{\infty} (\mathbf{M}_\infty)^\ell \mathbf{r}_z.$$

As established before, under the assumption $m_{zz} > 1$, we have $\mathbf{r}_z \ll \mathbf{0}$, hence, clearly, $\mathbf{s}'_z \ll \mathbf{0}$, and in particular

$$\frac{dS_z(\infty)}{dN_z} = \frac{ds_z}{dN_z} < 0.$$

This completes the proof. □

Proof of Theorem 4.4.12. *o Explicit expression of R_0 .* We first derive an explicit expression for R_0 by analysing the characteristic polynomial of $\mathbf{M}(\mathbf{N})$. Write $n := n_1 \in [0, 1]$, so $n_2 = 1 - n$. The next generation matrix then takes the form

$$\mathbf{M}(\mathbf{N}) = \begin{pmatrix} \tilde{m}_{11} n & \tilde{m}_{12} n \\ \tilde{m}_{21} (1 - n) & \tilde{m}_{22} (1 - n) \end{pmatrix}.$$

For $n \in (0, 1)$ all entries are strictly positive (since $\mathbf{K}^d \gg \mathbf{0}$ and $\mathbf{P} \gg \mathbf{0}$), and therefore $\mathbf{M}(\mathbf{N})$ is irreducible.

The characteristic polynomial of $\mathbf{M}(\mathbf{N})$ is

$$\lambda^2 - \text{tr}(\mathbf{M}(\mathbf{N}))\lambda + \det(\mathbf{M}(\mathbf{N})) = 0,$$

where

$$\operatorname{tr}(\mathbf{M}(\mathbf{N})) = \tilde{m}_{22} + n(\tilde{m}_{11} - \tilde{m}_{22}), \quad \det(\mathbf{M}(\mathbf{N})) = n(1-n)(\tilde{m}_{11}\tilde{m}_{22} - \tilde{m}_{12}\tilde{m}_{21}).$$

Hence the dominant eigenvalue is given by,

$$R_0(n) = \frac{1}{2} \left(\tilde{m}_{22} + n(\tilde{m}_{11} - \tilde{m}_{22}) + \sqrt{D(n)} \right), \quad (4.30)$$

with discriminant

$$D(n) := \operatorname{tr}(\mathbf{M}(\mathbf{N}))^2 - 4\det(\mathbf{M}(\mathbf{N})) = Un^2 + Vn + W, \quad (4.31)$$

and

$$U = (\tilde{m}_{11} + \tilde{m}_{22})^2 - 4\tilde{m}_{12}\tilde{m}_{21}, \quad V = 4\tilde{m}_{12}\tilde{m}_{21} - 2\tilde{m}_{22}(\tilde{m}_{11} + \tilde{m}_{22}), \quad W = \tilde{m}_{22}^2. \quad (4.32)$$

◦ *Differentiability on $[0, 1]$.* We now establish differentiability of R_0 on $n \in [0, 1]$. The only potential source of non-differentiability in (4.30) is the term $\sqrt{D(n)}$, so it suffices to show that $D(n) > 0$ for all $n \in [0, 1]$.

The discriminant $D(n)$ in (4.31) satisfies

$$D(n) = (\lambda_1(n) - \lambda_2(n))^2 \geq 0,$$

where $\lambda_1(n) \geq \lambda_2(n)$ are the two eigenvalues of $\mathbf{M}(\mathbf{N})$; this follows from the identities $\operatorname{tr}(\mathbf{M}(\mathbf{N})) = \lambda_1(n) + \lambda_2(n)$ and $\det(\mathbf{M}(\mathbf{N})) = \lambda_1(n)\lambda_2(n)$. For $n \in (0, 1)$ we have $\mathbf{M}(\mathbf{N}) \gg \mathbf{0}$, hence by Perron–Frobenius the dominant eigenvalue is simple and therefore $\lambda_1(n) \neq \lambda_2(n)$. Consequently $D(n) > 0$ on $(0, 1)$. At the endpoints, $D(0) = \tilde{m}_{22}^2 > 0$ and $D(1) = \tilde{m}_{11}^2 > 0$, so in fact $D(n) > 0$ on $[0, 1]$. Thus $n \mapsto \sqrt{D(n)}$ is differentiable on $[0, 1]$, and (4.30) implies that R_0 is differentiable on $[0, 1]$.

◦ *Derivative and its sign at $n \in \{0, \frac{1}{2}, 1\}$.* Differentiating (4.30) and using $D'(n) = 2Un + V$ gives, for $n \in [0, 1]$,

$$\frac{dR_0}{dn} = \frac{1}{2} \left(\tilde{m}_{11} - \tilde{m}_{22} + \frac{D'(n)}{2\sqrt{D(n)}} \right). \quad (4.33)$$

This expression simplifies at the three points of interest.

– At $n = 0$,

$$\left. \frac{dR_0}{dn} \right|_{n=0} = \frac{\tilde{m}_{12}\tilde{m}_{21} - \tilde{m}_{22}^2}{\tilde{m}_{22}},$$

so the sign equals the sign of $\tilde{m}_{12}\tilde{m}_{21} - \tilde{m}_{22}^2$.

– At $n = 1$,

$$\left. \frac{dR_0}{dn} \right|_{n=1} = \frac{\tilde{m}_{11}^2 - \tilde{m}_{12}\tilde{m}_{21}}{\tilde{m}_{11}},$$

so the sign equals the sign of $\tilde{m}_{11}^2 - \tilde{m}_{12}\tilde{m}_{21}$.

– At $n = \frac{1}{2}$,

$$\left. \frac{dR_0}{dn} \right|_{n=\frac{1}{2}} = \frac{(\tilde{m}_{11} - \tilde{m}_{22})(\tilde{m}_{11} + \tilde{m}_{22} + \sqrt{A})}{2\sqrt{A}}, \quad A := (\tilde{m}_{11} - \tilde{m}_{22})^2 + 4\tilde{m}_{12}\tilde{m}_{21}.$$

Since $A > 0$, we have $\sqrt{A} > 0$ and $\tilde{m}_{11} + \tilde{m}_{22} + \sqrt{A} > 0$. Hence the sign equals the sign of $\tilde{m}_{11} - \tilde{m}_{22}$.

◦ *At most one extremum.* We now show that R_0 has at most one extremum for $n \in [0, 1]$. If $\tilde{m}_{11} = \tilde{m}_{22}$, then (4.33) reduces to

$$\frac{dR_0}{dn} = \frac{D'(n)}{4\sqrt{D(n)}},$$

and since $D'(n)$ is linear in n , it has at most one zero. Hence R_0 has at most one extremum.

Assume now $\tilde{m}_{11} \neq \tilde{m}_{22}$. Setting (4.33) equal to zero and rearranging gives

$$\sqrt{D(n)} = \frac{D'(n)}{2(\tilde{m}_{22} - \tilde{m}_{11})}. \quad (4.34)$$

Since $\sqrt{D(n)} > 0$, any solution of (4.34) must satisfy

$$\text{sign}(D'(n)) = \text{sign}(\tilde{m}_{22} - \tilde{m}_{11}).$$

Squaring (4.34) yields a quadratic equation in n , and therefore it has at most two real solutions, say n_+ and n_- . For these solutions one obtains after squaring (4.34)

$$D'(n_{\pm}) = 2Un_{\pm} + V = \pm\sqrt{V^2 - 4UQ},$$

for a constant Q . In particular, $D'(n_+)$ and $D'(n_-)$ have opposite signs. Hence at most one of n_+ or n_- can satisfy the sign constraint imposed by (4.34). Consequently, (4.34) has at most one solution in $[0, 1]$, and therefore R_0 has at most one extremum on $[0, 1]$.

This proves the theorem. $\square$

4.6 Conclusion & discussion

In this chapter, we studied a deterministic multi-type SIR model in which the contact pattern $\mathbf{K}(\mathbf{N})$ depends explicitly on the demographic vector $\mathbf{N}$. Outbreak severity was quantified by the basic reproduction number $R_0 = \rho(\mathbf{M}(\mathbf{N}))$ and by the fractional final size $1 - \sigma$, characterised by the final-size equations. This framework makes the chain $\mathbf{N} \mapsto \mathbf{K}(\mathbf{N}) \mapsto (R_0, 1 - \sigma)$ (‘population structure’ to ‘interaction structure’ to ‘epidemic measures’) analytically tractable, and allows us to assess when homogeneous approximations can misrepresent epidemic severity under demographic change.

Our main qualitative finding is that demographic changes (e.g., changes in age, behaviour or geographical structure) can influence the severity of future epidemic outbreaks. Specifically, under a linear bilateral contact pattern in an ageing context (here, each young individual maintains a fixed number of contacts), a decrease in the proportion of young individuals reduces the fractional final size in every age group and lowers the basic reproduction number. Similar conclusions hold for the linear density dependent contact pattern.

The main message for policymakers is that demographic changes such as ageing can influence the severity of future epidemic outbreaks. When comparing a potential new outbreak

with one that occurred in the past, one should account for demographic changes to adjust predictions and, where required, the intervention strategy. Importantly, a lower final size or basic reproduction number does not necessarily imply a smaller public-health burden, as these measures do not take into account outcomes like hospitalisation and mortality.

We now discuss aspects that call for further attention. Our analysis uses a deterministic multi-type SIR framework, which is appropriate when populations are large enough for mean-field approximations; in small populations, however, there can be a substantial probability that an outbreak remains small even when $R_0 > 1$. Moreover, the SIR model is a rough simplification. Although the final size and basic reproduction number [90] are robust to many extensions (e.g., additional infectious states), models with high infection fatality may behave differently, particularly when disease-induced deaths alter the contact structure [46].

Our emphasis here has been qualitative. To assess quantitative impact, the natural next step is to identify and calibrate a demography dependent contact pattern for the population of interest. For example, to evaluate the linear bilateral contact pattern one could conduct a contact study in the spirit of [116] and estimate the parameters $(c_{ij})_{1 \leq i, j \leq m}$.

Doing so, however, brings practical modelling issues to the foreground. A drawback of multi-type SIR models is the larger number of parameters relative to a homogeneous SIR model. In particular, when m is large, an $m \times m$ contact matrix is difficult to estimate without rich data. This also raises an important model selection problem: how should one choose the partition into groups, and in particular the number of groups m ? From a statistical perspective, this problem is interesting in its own right, as it involves a trade-off between an overly coarse grouping (too few groups) and overfitting (too many groups).

More broadly, our results underline that demography is not just background context but a structural driver of transmission, and that recognising this link can support more realistic scenario planning and more resilient public-health decision-making.

4.A Mathematical Statements

In this appendix we prove several supporting lemmas and a canonical theorem which are used in the main text. Throughout this section, z denotes a scalar; $\mathbf{x}$ and $\mathbf{y}$ denote m -dimensional column vectors; $\mathbf{A} \in \mathbb{R}^{m \times m}$ is a positive irreducible matrix; and $\rho(\mathbf{A})$ denotes the dominant eigenvalue of $\mathbf{A}$.

Lemma 4.A.1. (i) $1 - e^{-z} \leq z$ for $z \geq 0$.

(ii) For $\varepsilon > 0$ there exists $\delta = \delta(\varepsilon) > 0$ such that $1 - e^{-z} \geq (1 - \varepsilon)z$ for $0 \leq z \leq \delta(\varepsilon)$.

(iii) $1 - e^{-\theta z} > \theta(1 - e^{-z})$ for $z > 0$ and $0 < \theta < 1$.

Proof. (i) Define $h(z) := 1 - e^{-z} - z$ for $z \geq 0$. Then $h(0) = 0$ and

$$h'(z) = e^{-z} - 1 \leq 0,$$

for $z \geq 0$. Hence h is nonincreasing on $[0, \infty)$, so $h(z) \leq h(0) = 0$, i.e. $1 - e^{-z} \leq z$ for all $z \geq 0$.

(ii) Fix $\varepsilon > 0$ and define

$$h(z) := 1 - e^{-z} - (1 - \varepsilon)z, \quad z \geq 0.$$

Then $h(0) = 0$ and

$$h'(z) = e^{-z} - (1 - \varepsilon), \quad \text{so } h'(0) = \varepsilon > 0.$$

Consequently, h is positive for small positive z .

(iii) Fix $z > 0$ and define, for $\theta \in [0, 1]$,

$$H(\theta) := 1 - e^{-\theta z} - \theta(1 - e^{-z}).$$

Then H is twice continuously differentiable, with $H(0) = H(1) = 0$, and

$$H'(\theta) = ze^{-\theta z} - (1 - e^{-z}), \quad H''(\theta) = -z^2 e^{-\theta z} < 0 \quad \text{for } \theta \in (0, 1).$$

So H is strictly concave on $[0, 1]$. Moreover,

$$H'(0) = z - (1 - e^{-z}) > 0$$

by the proof of part (i). A strictly concave function with $H(0) = H(1) = 0$ and $H'(0) > 0$ must satisfy $H(\theta) > 0$ for every $0 < \theta < 1$. Therefore $1 - e^{-\theta z} > \theta(1 - e^{-z})$ for $z > 0$ and $0 < \theta < 1$. $\square$

Theorem 4.A.2. Let $\mathbf{A} = (a_{ij})_{1 \leq i, j \leq m}$ be an irreducible matrix with strictly positive entries and let $F : \mathbb{R}_{\geq 0}^m \rightarrow \mathbb{R}_{\geq 0}^m$ be defined componentwise by

$$F_i(\mathbf{x}) := 1 - \exp(-(\mathbf{A}\mathbf{x})_i), \quad i = 1, \dots, m.$$

Consider the fixed point equation

$$\mathbf{x} = F(\mathbf{x}). \tag{4.35}$$

Then:

(i) F is order preserving: if $\mathbf{x} \geq \mathbf{y}$ (componentwise), then $F(\mathbf{x}) \geq F(\mathbf{y})$.

(ii) Equation (4.35) has at most one positive solution (i.e. at most one solution in $(0, \infty)^m$).

(iii) If $\rho(\mathbf{A}) \leq 1$, then (4.35) has no positive solution.

(iv) If $\rho(\mathbf{A}) > 1$, then (4.35) has a positive solution.

Proof. (i) Assume $\mathbf{x} \geq \mathbf{y}$. Since $\mathbf{A}$ has nonnegative entries, we have $\mathbf{A}\mathbf{x} \geq \mathbf{A}\mathbf{y}$, hence $(\mathbf{A}\mathbf{x})_i \geq (\mathbf{A}\mathbf{y})_i$ for each i . Therefore $e^{-(\mathbf{A}\mathbf{x})_i} \leq e^{-(\mathbf{A}\mathbf{y})_i}$, and hence

$$F_i(\mathbf{x}) = 1 - e^{-(\mathbf{A}\mathbf{x})_i} \geq 1 - e^{-(\mathbf{A}\mathbf{y})_i} = F_i(\mathbf{y}), \quad i = 1, \dots, m,$$

concluding $F(\mathbf{x}) \geq F(\mathbf{y})$.

(ii) We first show that any nonzero fixed point is automatically *strictly* positive in every component. Let $\mathbf{x} \geq \mathbf{0}$ solve (4.35) and assume $\mathbf{x} \neq \mathbf{0}$. Define the index set of positive components of $\mathbf{x}$:

$$P_+ := \{i \in \{1, \dots, m\} : x_i > 0\}.$$

For any subset $P \subset \{1, \dots, m\}$ define

$$\mathbf{A}P := \{i \in \{1, \dots, m\} : \exists j \in P \text{ such that } a_{ij} > 0\},$$

the set of indices that receive positive input from P after one multiplication by $\mathbf{A}$ (if one draws a graph induced by $\mathbf{A}$, then $\mathbf{A}P$ are the states that are reached by the states in P). Now take any $i \in \mathbf{A}P_+$. Then there exists $j \in P_+$ with $a_{ij} > 0$, hence

$$(\mathbf{A}\mathbf{x})_i = \sum_{k=1}^m a_{ik}x_k \geq a_{ij}x_j > 0.$$

Consequently $x_i = F_i(\mathbf{x}) = 1 - e^{-(\mathbf{A}\mathbf{x})_i} > 0$, so $i \in P_+$. We have shown $\mathbf{A}P_+ \subset P_+$. Iterating gives $\mathbf{A}^n P_+ \subset P_+$ for all $n \geq 1$.

Because $\mathbf{A}$ is irreducible and has strictly positive entries, from any nonempty set of indices one can reach every index in finitely many steps (equivalently: the directed graph of $\mathbf{A}$ is strongly connected). Since P_+ is nonempty (because $\mathbf{x} \neq \mathbf{0}$), the inclusions $\mathbf{A}^n P_+ \subset P_+$ force $P_+ = \{1, \dots, m\}$. Hence $x_i > 0$ for all i .

We now prove uniqueness. Suppose $\mathbf{x}$ and $\mathbf{y}$ are two positive solutions of (4.35). Define

$$\theta := \min_{1 \leq i \leq m} \frac{x_i}{y_i},$$

which is well-defined and strictly positive because all components are positive and the index set is finite. Assume for contradiction that $\theta < 1$ (if $\theta \geq 1$, interchange x and y in the definition of θ , if $\theta = 1$ we are done). Choose an index j such that $\theta = \frac{x_j}{y_j}$, so $x_j = \theta y_j$ and $\mathbf{x} \geq \theta \mathbf{y}$ componentwise.

Multiplying by $\mathbf{A} \geq 0$ preserves the inequality, hence $\mathbf{A}\mathbf{x} \geq \theta \mathbf{A}\mathbf{y}$. Now, using that $u \mapsto e^{-u}$ is decreasing, we obtain $e^{-(\mathbf{A}\mathbf{x})_j} \leq e^{-\theta(\mathbf{A}\mathbf{y})_j}$. Therefore,

$$x_j = F_j(\mathbf{x}) = 1 - e^{-(\mathbf{A}\mathbf{x})_j} \geq 1 - e^{-\theta(\mathbf{A}\mathbf{y})_j}.$$

Since $(\mathbf{A}\mathbf{y})_j > 0$ and $0 < \theta < 1$, Lemma 4.A.1(iii) yields the strict inequality

$$1 - e^{-\theta(\mathbf{A}\mathbf{y})_j} > \theta(1 - e^{-(\mathbf{A}\mathbf{y})_j}) = \theta F_j(\mathbf{y}) = \theta y_j,$$

and hence $x_j > \theta y_j$, contradicting $x_j = \theta y_j$. This proves that there is at most one positive solution.

(iii) Assume for contradiction that $\mathbf{x}$ is a positive solution of (4.35) and $\rho(\mathbf{A}) \leq 1$. By Lemma 4.A.1(i), for each i ,

$$x_i = 1 - e^{-(\mathbf{A}\mathbf{x})_i} \leq (\mathbf{A}\mathbf{x})_i,$$

so $\mathbf{x} \leq \mathbf{A}\mathbf{x}$. Iterating yields

$$\mathbf{x} \leq \mathbf{A}^n \mathbf{x} \quad \text{for all } n \geq 1. \tag{4.36}$$

First consider $\rho(\mathbf{A}) < 1$. Use the operator norm associated with $\|\cdot\|_\infty$, namely

$$\|\mathbf{x}\|_\infty := \max_i |x_i|, \quad \|\mathbf{A}\|_\infty := \sup_{\mathbf{x} \neq \mathbf{0}} \frac{\|\mathbf{Ax}\|_\infty}{\|\mathbf{x}\|_\infty}.$$

Then $\|\mathbf{Ax}\|_\infty \leq \|\mathbf{A}\|_\infty \|\mathbf{x}\|_\infty$ and $\|\mathbf{A}^n\|_\infty$ is submultiplicative, so by Gelfand's formula $\lim_{n \rightarrow \infty} \|\mathbf{A}^n\|_\infty^{1/n} = \rho(\mathbf{A})$. Pick $\varepsilon > 0$ such that $\rho(\mathbf{A}) + \varepsilon < 1$. Then there exists $N(\varepsilon)$ with $\|\mathbf{A}^n\|_\infty \leq (\rho(\mathbf{A}) + \varepsilon)^n$ for all $n \geq N(\varepsilon)$. Hence

$$\|\mathbf{A}^n \mathbf{x}\|_\infty \leq \|\mathbf{A}^n\|_\infty \|\mathbf{x}\|_\infty \leq (\rho(\mathbf{A}) + \varepsilon)^n \|\mathbf{x}\|_\infty,$$

for $n \geq N(\varepsilon)$. On the other hand, (4.36) implies $\|\mathbf{A}^n \mathbf{x}\|_\infty \geq \|\mathbf{x}\|_\infty$. Combining gives

$$\|\mathbf{x}\|_\infty \leq (\rho(\mathbf{A}) + \varepsilon)^n \|\mathbf{x}\|_\infty.$$

Now noting that $\rho(\mathbf{A}) + \varepsilon < 1$, this forces $\|\mathbf{x}\|_\infty = 0$ in order to satisfy the inequality for large n , contradicting positivity of $\mathbf{x}$.

Now consider $\rho(\mathbf{A}) = 1$. From part (ii) we already know that a nonzero fixed point must satisfy $x_i > 0$ for all i . Choose a constant $\underline{x}$ such that

$$0 < \underline{x} < \min_{1 \leq i \leq m} x_i.$$

Define $g(z) := 1 - e^{-z} - z$ for $z \geq 0$. Then $g'(z) = e^{-z} - 1 < 0$ for $z > 0$, so g is strictly decreasing. Hence for all $z > \underline{x}$ we have $g(z) < g(\underline{x})$, i.e.

$$1 - e^{-z} - z < 1 - e^{-\underline{x}} - \underline{x},$$

or equivalently,

$$1 - e^{-z} < z - p,$$

where we set

$$p := \underline{x} - (1 - e^{-\underline{x}}) > 0,$$

using Lemma 4.A.1(i) strictly since $\underline{x} > 0$.

Next, for each i we have by Lemma 4.A.1(i) that

$$x_i = 1 - e^{-(\mathbf{Ax})_i} \leq (\mathbf{Ax})_i.$$

Since $x_i > \underline{x}$, this implies $(\mathbf{Ax})_i > \underline{x}$ for every i . Thus we may apply the inequality above with $z = (\mathbf{Ax})_i$ to obtain

$$x_i = 1 - e^{-(\mathbf{Ax})_i} < (\mathbf{Ax})_i - p,$$

or equivalently

$$\mathbf{Ax} \geq \mathbf{x} + p \mathbf{1}. \quad (4.37)$$

Let $\mathbf{y}^* > \mathbf{0}$ be the (left) Perron eigenvector corresponding to $\rho(\mathbf{A}) = 1$, so $\mathbf{y}^{*\top} \mathbf{A} = \mathbf{y}^{*\top}$. Left-multiplying (4.37) by $\mathbf{y}^{*\top}$ gives

$$\mathbf{y}^{*\top} \mathbf{x} = \mathbf{y}^{*\top} \mathbf{Ax} \geq \mathbf{y}^{*\top} \mathbf{x} + p \mathbf{y}^{*\top} \mathbf{1},$$

which is impossible because $p > 0$ and $\mathbf{y}^{*\top} \mathbf{1} > 0$. This contradiction shows that no positive fixed point can exist when $\rho(\mathbf{A}) = 1$. Together with the previous case, this proves (iii).

(iv) Assume $\rho(\mathbf{A}) > 1$. Let $\mathbf{y} \gg \mathbf{0}$ be the right Perron eigenvector, $\mathbf{A}\mathbf{y} = \rho(\mathbf{A})\mathbf{y}$. Scale $\mathbf{y}$ such that $\max_j y_j = \rho(\mathbf{A})^{-1}$, so that $\rho(\mathbf{A})y_j \leq 1$ for every j .

Choose $\varepsilon \in (0, 1)$ such that $(1 - \varepsilon)\rho(\mathbf{A}) > 1$. Let $\delta = \delta(\varepsilon) > 0$ be as in Lemma 4.A.1(ii). For each component j we have $0 \leq \delta\rho(\mathbf{A})y_j \leq \delta$, hence Lemma 4.A.1(ii) applies with $z = \delta\rho(\mathbf{A})y_j$ and yields

$$F_j(\delta\mathbf{y}) = 1 - e^{-(\mathbf{A}(\delta\mathbf{y}))_j} = 1 - e^{-\delta(\mathbf{A}\mathbf{y})_j} = 1 - e^{-\delta\rho(\mathbf{A})y_j} \geq (1 - \varepsilon)\delta\rho(\mathbf{A})y_j \geq \delta y_j.$$

Thus

$$F(\delta\mathbf{y}) \geq \delta\mathbf{y}. \quad (4.38)$$

Define the iterative sequence

$$\mathbf{x}^{(0)} := \delta\mathbf{y}, \quad \mathbf{x}^{(n+1)} := F(\mathbf{x}^{(n)}), \quad n \geq 0.$$

Then (4.38) gives $\mathbf{x}^{(1)} \geq \mathbf{x}^{(0)}$. Using part (i) (order preservation), an induction shows that $\mathbf{x}^{(n+1)} \geq \mathbf{x}^{(n)}$ for all n , i.e. the sequence is componentwise nondecreasing.

Moreover, $0 \leq F_i(\mathbf{x}) \leq 1$ for all $\mathbf{x} \geq \mathbf{0}$, hence $\mathbf{x}^{(n)} \leq \mathbf{1}$ for all n . So $\{\mathbf{x}^{(n)}\}$ is monotone increasing and bounded above, and therefore converges componentwise to a limit $\mathbf{x}^{(\infty)} \in [0, 1]^m$.

Finally, F is continuous, so passing to the limit in $\mathbf{x}^{(n+1)} = F(\mathbf{x}^{(n)})$ yields

$$\mathbf{x}^{(\infty)} = F(\mathbf{x}^{(\infty)}),$$

i.e. $\mathbf{x}^{(\infty)}$ is a fixed point. Since $\mathbf{x}^{(0)} = \delta\mathbf{y} > \mathbf{0}$ and the sequence is nondecreasing, we have $\mathbf{x}^{(\infty)} \geq \mathbf{x}^{(0)} > \mathbf{0}$, so the fixed point is positive. This proves (iv). $\square$

Lemma 4.A.3. Assume that $\rho(\mathbf{A}) > 1$ and let $\mathbf{x} \in (0, 1)^m$ be the (unique) solution of the fixed point equation $\mathbf{x} = F(\mathbf{x})$ (that follows from Theorem 4.A.2). Define the matrix $\tilde{\mathbf{A}} = (\tilde{a}_{ij})_{1 \leq i, j \leq m}$ by

$$\tilde{a}_{ij} := (1 - x_i)a_{ij}.$$

Then $\rho(\tilde{\mathbf{A}}) < 1$.

Proof. From $x_i = 1 - \exp(-(\mathbf{A}\mathbf{x})_i)$ we obtain $1 - x_i = \exp(-(\mathbf{A}\mathbf{x})_i)$, hence $\log(1 - x_i) + (\mathbf{A}\mathbf{x})_i = 0$. Multiplying by $(1 - x_i)$ gives

$$(1 - x_i) \log(1 - x_i) + (1 - x_i)(\mathbf{A}\mathbf{x})_i = 0.$$

By definition of $\tilde{\mathbf{A}}$, the second term is precisely the i th component of $\tilde{\mathbf{A}}\mathbf{x}$. Therefore, for $i = 1, \dots, m$,

$$(1 - x_i) \log(1 - x_i) + (\tilde{\mathbf{A}}\mathbf{x})_i = 0. \quad (4.39)$$

Since $\mathbf{x} \in (0, 1)^m$, the terms $(1 - x_i)$ are strictly positive, and thus $\tilde{\mathbf{A}}$ is nonnegative and has the same zero pattern (hence the same irreducibility property) as $\mathbf{A}$. Let $\mathbf{y}^* \gg \mathbf{0}$ be a left Perron eigenvector of $\tilde{\mathbf{A}}$, corresponding to $\rho(\tilde{\mathbf{A}})$, i.e.

$$\mathbf{y}^{*\top} \tilde{\mathbf{A}} = \rho(\tilde{\mathbf{A}}) \mathbf{y}^{*\top}.$$

Assume, for contradiction, that $\rho(\tilde{\mathbf{A}}) \geq 1$. Define for $0 \leq z < 1$, $h(z) := (1 - z) \log(1 - z) + \rho(\tilde{\mathbf{A}})z$. Then $h(0) = 0$ and for $0 < z < 1$, $h'(z) = -\log(1 - z) - 1 + \rho(\tilde{\mathbf{A}})$. Because $-\log(1 - z) > 0$ for $0 < z < 1$ and $\rho(\tilde{\mathbf{A}}) - 1 \geq 0$, we have $h'(z) > 0$ on $(0, 1)$. Hence h is strictly increasing on $[0, 1)$, and in particular $h(z) > 0$ for $z \in (0, 1)$.

Now multiply (4.39) by y_i^* and sum over i . Using the eigenvector relation,

$$\sum_{i=1}^m y_i^* (\tilde{\mathbf{A}}\mathbf{x})_i = \mathbf{y}^{*\top} \tilde{\mathbf{A}}\mathbf{x} = \rho(\tilde{\mathbf{A}}) \mathbf{y}^{*\top} \mathbf{x} = \sum_{i=1}^m \rho(\tilde{\mathbf{A}}) y_i^* x_i,$$

we obtain

$$0 = \sum_{i=1}^m y_i^* [(1 - x_i) \log(1 - x_i)] + \sum_{i=1}^m \rho(\tilde{\mathbf{A}}) y_i^* x_i = \sum_{i=1}^m y_i^* h(x_i).$$

But $y_i^* > 0$ and $h(x_i) > 0$ for every i (since $x_i \in (0, 1)$), so the right-hand side is strictly positive, a contradiction. Therefore our assumption $\rho(\tilde{\mathbf{A}}) \geq 1$ is false, and we conclude that $\rho(\tilde{\mathbf{A}}) < 1$. $\square$